STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 118581

To: Terra Gibbs **Location:** REM/2D10/2C18 **Art Unit:** 1635 **Wednesday, April 07, 2004** **Case Serial Number:** 10/033243	**From:** Beverly Shears **Location:** Remsen Bldg. RM 1A54 **Phone:** 571-272-2528 beverly.shears@uspto.gov

Search Notes

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STIC-Biotech/ChemLib 118581

From: Gibbs, Terra
Sent: Friday, April 02, 2004 2:33 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search...

Can you please do a search of SEQ ID NO:132 of USSN 10/033,243 in all regular and commercial databases?

Terra Cotta Gibbs, Ph.D.
Art Unit 1635
Remsen Building 2D10
571-272-0758

Searcher:_____
Phone:_____
Location:_____
Date Picked Up:_____
Date Completed:_____
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences:_____
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.:_____
WWW/Internet:_____
Other (specify):_____

U.S. DEPARTMENT OF COMMERCE
Patent and Trademark Office

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____

Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

STAFF USE ONLY

Date completed: 04-06-04
Searcher: Beverly C 2528
Terminal time: 2½
Elapsed time: _____
CPU time: _____
Total time: 25
Number of Searches: _____
Number of Databases: 2

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
✓ STN
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_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ Other CGN

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FILE 'REGISTRY' ENTERED AT 08:18:30 ON 06 APR 2004
L1 26 S TCGTCGAACGTTCGAGATGAT/SQSN

FILE 'HCAPLUS' ENTERED AT 08:19:36 ON 06 APR 2004
L2 7 S L1

L2 ANSWER 1 OF 7 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 22 Feb 2004
ACCESSION NUMBER: 2004:142919 HCAPLUS
DOCUMENT NUMBER: 140:198064
TITLE: Particulate immunostimulant
INVENTOR(S): Van Nest, Gary; Tuck, Stephen
PATENT ASSIGNEE(S): Dynavax Technologies Corporation, USA
SOURCE: PCT Int. Appl., 90 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004014322	A2	20040219	WO 2003-US25415	20030812

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2002-402968P P 20020812

AB The authors disclose immunomodulatory compns. which comprise a cationic condensing agent, an immunomodulatory compound, and a stabilizing agent. The compns. of the invention typically form particles which have increased immunomodulatory activity as compared to immunomodulatory compds. not formulated in the compns. of the invention. Also provided are methods of making the compns. and methods for therapeutic use of the compns. In one example, interferon-γ release by human mononuclear cells was shown to be enhanced by the combination of CpG oligonucleotide, polymyxin B, and Tween-80.

IT **662376-82-1**
RL: PRP (Properties)
(unclaimed sequence; particulate immunostimulant)

L2 ANSWER 2 OF 7 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 15 Dec 2003
ACCESSION NUMBER: 2003:975836 HCAPLUS
DOCUMENT NUMBER: 140:75912
TITLE: IL-10 regulates plasmacytoid dendritic cell response to CpG-containing immunostimulatory sequences

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AUTHOR(S): Duramad, Omar; Fearon, Karen L.; Chan, Jean H.; Kanzler, Holger; Marshall, Jason D.; Coffman, Robert L.; Barrat, Franck J.
CORPORATE SOURCE: Dynavax Technologies Corporation, Berkeley, CA, USA
SOURCE: Blood (2003), 102(13), 4487-4492
CODEN: BLOOAW; ISSN: 0006-4971
PUBLISHER: American Society of Hematology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Immunostimulatory sequences (ISS) are short oligonucleotides containing unmethylated cytosine-phosphate-guanine (CpG) dinucleotides that stimulate innate immune responses through Toll-like receptor-9 on B cells and plasmacytoid dendritic cell (PDC) precursors. The anti-inflammatory cytokine interleukin (IL)-10 is predicted to be a potent inhibitor of many of the activities described for ISS, and this may impact the use of ISS in disease states characterized by elevated IL-10. As the activities of ISS on PDCs are central to many clin. applications of ISS, we have studied the effects of IL-10 on PDC stimulation by 3 distinct classes of ISS. IL-10 inhibited cytokine production and survival of ISS-activated PDCs; however, IL-12 induction was much more sensitive to inhibition than interferon (IFN)-α induction. Within the PDC population are cells that respond to ISS by producing either IL-12 or IFN-α but not both cytokines. IL-12-producing PDCs require costimulation through CD40 and appear more mature than IFN-α-producing PDCs. The 3 distinct classes of ISS differed with respect to induction of PDC maturation and T-cell priming capacity. IL-10 regulated PDC activation but did not inhibit the subsequent T-cell-priming ability of PDCs already activated by ISS.

IT **640803-45-8**
RL: BSU (Biological study, unclassified); PAC (Pharmacological activity); BIOL (Biological study)
(IL-10 regulates plasmacytoid dendritic cell response to CpG-containing immunostimulatory sequences)

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 7 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 05 Dec 2003
ACCESSION NUMBER: 2003:950038 HCAPLUS
DOCUMENT NUMBER: 140:26897
TITLE: Chimeric immunomodulatory compounds comprising two or more nucleic acid moieties and non-nucleic acid spacer
INVENTOR(S): Fearon, Karen L.; Dina, Dino; Tuck, Stephen F.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 96 pp., Cont.-in-part of U.S. Ser. No. 176,883.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003225016	A1	20031204	US 2002-328578	20021223
US 2003175731	A1	20030918	US 2002-176883	20020621
US 2003199466	A1	20031023	US 2002-177826	20020621

PRIORITY APPLN. INFO.:
US 2001-299883P P 20010621
US 2002-375253P P 20020423
US 2002-176883 A2 20020621
US 2002-177826 A2 20020621

AB The invention provides immunomodulatory compds. and methods for immunomodulation of individuals using the immunomodulatory compds. The immunomodulatory compds. comprise two or more nucleic acid moieties and a non-nucleic acid spacer moiety. The nucleic acid contains e.g. 5'-CG-3', 5'-TCG-3', 5'-TCGA-3', 5'-TCGACGT-3', or 5'-TCGACGA-3'; and the non-nucleic acid is an oligoethylene glycol such as hexaethylene glycol. The chimeric compds. are incorporated into endotoxin-free compns. comprising antigen, pharmaceutically acceptable excipient, and optionally a cationic microsphere for modulating immune response.

IT **631925-51-4P 631925-64-9P 631926-21-1P 631926-36-8P**
RL: PRP (Properties); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(chimeric immunomodulatory compds. comprising two or more nucleic acid moieties and non-nucleic acid spacer)

L2 ANSWER 4 OF 7 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 01 Jul 2003
ACCESSION NUMBER: 2003:499872 HCAPLUS
DOCUMENT NUMBER: 139:99590
TITLE: Rational design of new CpG oligonucleotides that combine B cell activation with high IFN-α induction in plasmacytoid dendritic cells
AUTHOR(S): Hartmann, Gunther; Battiany, Julia; Poeck, Hendrik; Wagner, Moritz; Kerkmann, Miren; Lubenow, Norbert; Rothenfusser, Simon; Endres, Stefan
CORPORATE SOURCE: Department of Internal Medicine, Division of Clinical Pharmacology, Ludwig-Maximilians-University of Munich, Munich, Germany
SOURCE: European Journal of Immunology (2003), 33(6), 1633-1641
CODEN: EJIMAF; ISSN: 0014-2980
PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Two different types of CpG motif-containing oligonucleotides (CpG ODN) have been described: CpG-A with high induction of IFN-α in plasmacytoid dendritic cells; and CpG-B with little induction of IFN-α, but potent activation of B cells. In this study, we demonstrate that CpG-A fail to activate B cells unless plasmacytoid dendritic cells are present. We identified a new set of CpG ODN sequences which induces high levels of IFN-α in plasmacytoid dendritic cells but remains capable of directly activating B cells. These new CpG ODN (termed CpG-C) are more potent stimulants of B cells than CpG-B due to their ability of directly and indirectly

(via plasmacytoid dendritic cells) activating B cells. The sequence of CpG-C combines structural elements of both CpG-A and CpG-B. The most potent sequence, M362, contains a 5'-end "TCGTCG-motif" and a "GTCGTT-motif", both of which are present in CpG-B (ODN 2006); a palindromic sequence characteristic for CpG-A (ODN 2216); but no poly G motif required for CpG-A. In conclusion, we defined the first CpG-containing sequences that potently activate both TLR9-expressing immune cell subsets in humans, the plasmacytoid dendritic cell and the B cell. CpG-C may allow for improved therapeutic immuno-modulation in vivo.

IT **557124-76-2P**
RL: BSU (Biological study, unclassified); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation)
(rational design of new CpG oligonucleotides that combine B cell activation with high IFN-α induction in plasmacytoid dendritic cells)

REFERENCE COUNT: 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 5 OF 7 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 13 Jun 2003
ACCESSION NUMBER: 2003:453345 HCAPLUS
DOCUMENT NUMBER: 139:83598
TITLE: Identification of a novel CpG DNA class and motif that optimally stimulate B cell and plasmacytoid dendritic cell functions
AUTHOR(S): Marshall, Jason D.; Fearon, Karen; Abbate, Christi; Subramanian, Sandhya; Yee, Priscilla; Gregorio, Josh; Coffman, Robert L.; Van Nest, Gary
CORPORATE SOURCE: Dynavax Technologies Corporation, Berkeley, CA, USA
SOURCE: Journal of Leukocyte Biology (2003), 73(6), 781-792
CODEN: JLBIE7; ISSN: 0741-5400
PUBLISHER: Federation of American Societies for Experimental Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Recent reports have identified two major classes of CpG motif-containing oligodeoxynucleotide immunostimulatory sequences (ISS): uniformly modified phosphorothioate (PS) oligodeoxyribonucleotides (ODNs), which initiate B cell functions but poorly activate dendritic cells (DCs) to make interferon (IFN)-α, and chimeric PS/phospho diester (PO) ODNs containing runs of six contiguous guanosines, which induce very high levels of plasmacytoid DC (PDC)-derived IFN-α but poorly stimulate B cells. The authors have generated the first reported ISS, C274, which exhibits very potent effects on all human immune cells known to recognize ISS. C274 is a potent inducer of IFN-γ/IFN-α from peripheral blood mononuclear cells and exhibits accelerated kinetics of activity compared with standard ISS. This ODN also effectively stimulates B cells to proliferate, secrete cytokines, and express costimulatory antigens. In addition, C274 specifically activates PDCs to undergo maturation and secrete cytokines, including very high levels of IFN-α. Sequence

variation studies based on C274 were used to identify the general motif requirements for this novel and distinct class of ISS. In contrast, chimeric PO/PS CpG-containing ODNs with Poly guanosine sequences exert a differential pattern of ISS activity compared with C274, perhaps in part as a result of their greatly different structural nature. This pattern is composed of high IFN-α/IFN-γ induction and low DC maturation in the absence of B cell stimulation. In conclusion, the authors have generated a novel class of ISS that transcends the limitations ascribed to classes described previously in that it provides excellent stimulation of B cells and simultaneously activates PDCs to differentiate and secrete large amts. of type I IFN.

IT **554470-62-1P**
RL: BSU (Biological study, unclassified); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation)
(identification of a novel CpG DNA class and motif that optimally stimulate B cell and plasmacytoid dendritic cell functions)

REFERENCE COUNT: 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 6 OF 7 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 05 Jan 2003
ACCESSION NUMBER: 2003:6160 HCAPLUS
DOCUMENT NUMBER: 138:88635
TITLE: Chimeric immunomodulatory compounds comprising nucleic acids linked through dendrimer or polysaccharide spacer and antigen for treating allergy, infection or cancer
INVENTOR(S): Fearon, Karen L.; Dina, Dino; Tuck, Stephen F.
PATENT ASSIGNEE(S): Dynavax Technologies Corporation, USA
SOURCE: PCT Int. Appl., 224 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003000922	A2	20030103	WO 2002-US20025	20020621
WO 2003000922	A3	20031023		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2001-299883P P 20010621
US 2002-375253P P 20020423

AB The invention provides immunomodulatory compds. (CIC) and methods

for immunomodulation of individuals using the immunomodulatory compds. The CIC comprises one or more nucleic acid moieties and one or more non-nucleic acid moieties such as dendrimer, polysaccharide, and crosslinked polysaccharide through phosphodiester, phosphorothioate ester, phosphorodithioate ester, and other linkages. The CIC is capable of stimulating production of interferon γ and α by human peripheral blood mononuclear cells, as well as human B cell proliferation. Endotoxin-free compns. comprising the CIC covalently or non-covalently conjugated with antigen and cationic microsphere are useful for treating disorders associated with IgE or Th2-type immune response such as allergy, asthma, infection, viral infection, idiopathic pulmonary fibrosis, and cancer.

IT **482661-47-2P 482663-36-5P 482663-37-6P 482663-46-7P 482663-95-6P 482663-96-7P 482663-97-8P 483382-56-5P 483382-57-6P 483382-58-7P 483382-59-8P 483382-64-5P 483382-65-6P 483382-66-7P 483382-67-8P 483382-68-9P**
RL: PAC (Pharmacological activity); PRP (Properties); PUR (Purification or recovery); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(chimeric immunomodulatory compds. comprising nucleic acids linked through dendrimer or polysaccharide spacer and antigen for treating allergy, infection or cancer)

L2 ANSWER 7 OF 7 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 05 Jul 2002
ACCESSION NUMBER: 2002:504922 HCAPLUS
DOCUMENT NUMBER: 137:73254
TITLE: Immunomodulatory oligonucleotides containing immunostimulatory sequences for treatment of disorders associated with a Th2-type immune response
INVENTOR(S): Fearon, Karen L.; Dina, Dino
PATENT ASSIGNEE(S): Dynavax Technologies Corporation, USA
SOURCE: PCT Int. Appl., 95 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002052002	A2	20020704	WO 2001-US50821	20011227
WO 2002052002	A3	20030904		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,

CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2003049266 A1 20030313 US 2001-33243 20011227
EP 1364010 A2 20031126 EP 2001-991610 20011227
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRIORITY APPLN. INFO.: US 2000-258675P P 20001227
WO 2001-US50821 W 20011227
OTHER SOURCE(S): MARPAT 137:73254

AB The invention provides immunomodulatory polynucleotides and methods for immunomodulation of individuals using the immunomodulatory polynucleotides. Each immunomodulatory polynucleotide comprises at lease one immunostimulatory sequence (ISS). Thus, administration of 5'-tgactgtgaazgtttzgagatga-3' (where z = 5-bromocytosine) in conjunction with hepatitis B surface antigen (HBsAg) to baboons resulted in increased titers of anti-HBsAg antibodies as compared to administration of HBsAg alone or to administration of HBsAg with a non-ISS oligonucleotide. Complexation of immunomodulatory polynucleotides with cationic poly(lactic acid,glycolic acid) microspheres in a human PBMC assay showed significantly enhanced induction of interferon α and interferon γ in comparison to the polynucleotides alone.

IT **439891-56-2**
RL: PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(immunomodulatory oligonucleotides containing immunostimulatory sequences for treatment of disorders associated with a Th2-type immune response)

E1 THROUGH E25 ASSIGNED

FILE 'REGISTRY' ENTERED AT 08:20:19 ON 06 APR 2004
L3 25 SEA FILE=REGISTRY ABB=ON PLU=ON (439891-56-2/BI OR 482661-47-2/BI OR 482663-36-5/BI OR 482663-37-6/BI OR 482663-46-7/BI OR 482663-95-6/BI OR 482663-96-7/BI OR 482663-97-8/BI OR 483382-56-5/BI OR 483382-57-6/BI OR 483382-58-7/BI OR 483382-59-8/BI OR 483382-64-5/BI OR 483382-65-6/BI OR 483382-66-7/BI OR 483382-67-8/BI OR 483382-68-9/BI OR 554470-62-1/BI OR 557124-76-2/BI OR 631925-51-4/BI OR 631925-64-9/BI OR 631926-21-1/BI OR 631926-36-8/BI OR 640803-45-8/BI OR 662376-82-1/BI)

L4 25 L1 AND L3

L4 ANSWER 1 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **662376-82-1** REGISTRY
CN DNA, d(T-C-G-T-C-G-A-A-C-G-T-T-C-G-A-G-A-T-G-A-T) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 137: PN: WO2004014322 PAGE: 24 unclaimed sequence
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
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HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 140:198064

L4 ANSWER 2 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **640803-45-8** REGISTRY
CN DNA, d(P-thio)(T-C-G-T-C-G-A-A-C-G-T-T-C-G-A-G-A-T-G-A-T) (9CI) (CA INDEX NAME)
CI MAN
SQL 21

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HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 140:75912

L4 ANSWER 3 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **631926-36-8** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-A-sp-T), 3'-[O-(6-aminohexyl) hydrogen phosphorothioate] (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
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HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 140:26897

L4 ANSWER 4 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **631926-21-1** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,3-propanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,3-propanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-A-sp-T), 3'-[O-(14-hydroxy-5-mercapto-5-oxido-4,6-dioxa-10,11-dithia-5-phosphatetradec-1-yl) hydrogen phosphorothioate] (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t

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HITS AT:    1-21

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

REFERENCE   1:  140:26897

L4   ANSWER 5 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
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     propanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-
     A-sp-T), 5'-[O-(6-mercaptohexyl) hydrogen phosphorothioate] (9CI)
     (CA INDEX NAME)
CI   MAN
SQL  21

SEQ      1 tcgtcgaacg ttcgagatga t
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HITS AT:    1-21

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

REFERENCE   1:  140:26897

L4   ANSWER 6 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
RN   631925-51-4  REGISTRY
CN   DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)o
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     idene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-
     G[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-
     ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-
     1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-
     sp-A-sp-T) (9CI)  (CA INDEX NAME)
CI   MAN
SQL  21

SEQ      1 tcgtcgaacg ttcgagatga t
           ========== ========== =
HITS AT:    1-21

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

REFERENCE   1:  140:26897

L4   ANSWER 7 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
RN   557124-76-2  REGISTRY
CN   DNA, d(P-thio)(T-C-G-T-C-G-A-A-C-G-T-T-C-G-A-G-A-T-G-A-T) (9CI)  (CA
     INDEX NAME)
CI   MAN
SQL  21

SEQ      1 tcgtcgaacg ttcgagatga t
           ========== ========== =
```

HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:99590

L4 ANSWER 8 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **554470-62-1** REGISTRY
CN DNA, d(P-thio)(T-C-G-T-C-G-A-A-C-G-T-T-C-G-A-G-A-T-G-A-T) (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:83598

L4 ANSWER 9 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **483382-68-9** REGISTRY
CN Poly(oxy-1,2-ethanediyl), α-hydro-ω-hydroxy-, ester with 2'-deoxy-P-thioadenylyl-(3'→5')-2'-deoxy-P-thiocytidylyl-(3'→5')-2'-deoxy-P-thioguanylyl-(3'→5')-P-thiothymidylyl-(3'→5')-P-thiothymidylyl-(3'→5')-2'-deoxy-P-thiocytidylyl-(3'→5')-2'-deoxyguanosine 3',5'-bis(dihydrogen phosphorothioate), 2'-deoxy-P-thioadenylyl-(3'→5')-2'-deoxy-P-thioguanylyl-(3'→5')-2'-deoxy-P-thioadenylyl-(3'→5')-P-thiothymidylyl-(3'→5')-2'-deoxy-P-thioguanylyl-(3'→5')-2'-deoxy-P-thioadenylyl-(3'→5')-thymidine 5'-(dihydrogen phosphorothioate) and P-thiothymidylyl-(3'→5')-2'-deoxy-P-thiocytidylyl-(3'→5')-2'-deoxy-P-thioguanylyl-(3'→5')-P-thiothymidylyl-(3'→5')-2'-deoxy-P-thiocytidylyl-(3'→5')-2'-deoxy-P-thioguanylyl-(3'→5')-2'-deoxyadenosine 3'-(dihydrogen phosphorothioate) (2:1:1:1) (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 10 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **483382-67-8** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-

This Page Blank (uspto)

sp-A-sp-T-sp-G-sp-A-sp-T) (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 11 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **483382-66-7** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,6-hexanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,6-hexanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-A-sp-T) (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 12 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **483382-65-6** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,4-butanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,4-butanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-A-sp-T) (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 13 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **483382-64-5** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,3-propanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,3-propanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-A-sp-T), 5'-[O-[6-[(6-hydroxyhexyl)dithio]hexyl] hydrogen phosphorothioate] (9CI) (CA INDEX NAME)

CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 14 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **483382-59-8** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-A-sp-T), 3'-[O-(3-mercaptopropyl) hydrogen phosphorothioate] (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 15 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **483382-58-7** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,3-propanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,3-propanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-A-sp-T), 3'-[O-[3-(3-mercaptopropoxy)propyl] hydrogen phosphorothioate] (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 16 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **483382-57-6** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-

ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinyl
idene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-
G[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-
ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-
1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-
sp-A-sp-T), 5'-[O-(6-mercaptohexyl) hydrogen phosphorothioate] (9CI)
(CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 17 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **483382-56-5** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)o
xy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-
ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinyl
idene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-
G[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-
ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-
1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-
sp-A-sp-T), 5'-[O-[6-[(6-hydroxyhexyl)dithio]hexyl] hydrogen
phosphorothioate] (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 18 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **482663-97-8** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)o
xy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-
ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinyl
idene)oxy-1,3-propanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-
sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,2-
ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-
1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-
G-sp-A-sp-T-sp-G-sp-A-sp-T) (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 19 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **482663-96-7** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-A-sp-T), 3'-[O-[3-[(3-hydroxypropyl)dithio]propyl] hydrogen phosphorothioate] (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 20 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **482663-95-6** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,3-propanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,3-propanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-A-sp-T), 3'-[O-[3-[3-[(3-hydroxypropyl)dithio]propoxy]propyl] hydrogen phosphorothioate] (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 21 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **482663-46-7** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,3-propanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,3-propanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-A-sp-T), 5'-[O-(6-mercaptohexyl) hydrogen phosphorothioate] (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 22 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **482663-37-6** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,3-propanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,3-propanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-A-sp-T) (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 23 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **482663-36-5** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-A-sp-T) (9CI) (CA INDEX NAME)
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:88635

L4 ANSWER 24 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **482661-47-2** REGISTRY
CN DNA, d(T-sp-C-sp-G-sp-T-sp-C-sp-G-sp-A[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-C-sp-G-sp-T-sp-T-sp-C-sp-G[oxy(mercaptophosphinylidene)oxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-1,2-ethanediyloxy-

1,2-ethanediyloxy(mercaptophosphinylidene)oxy]A-sp-G-sp-A-sp-T-sp-G-sp-A-sp-T), 3',3''',3'''''-[O,O',O''-[nitrilotris[2,1-ethanediyl(2,5-dioxo-1,3-pyrrolidinediyl)thio-3,1-propanediyl]] tris(hydrogen phosphorothioate)] (9CI) (CA INDEX NAME)
CI MAN
SQL 63,21,21,21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

REFERENCE 1: 138:88635

L4 ANSWER 25 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
RN **439891-56-2** REGISTRY
CN DNA, d(T-C-G-T-C-G-A-A-C-G-T-T-C-G-A-G-A-T-G-A-T) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 132: PN: WO02052002 SEQID: 132 claimed DNA
CI MAN
SQL 21

SEQ 1 tcgtcgaacg ttcgagatga t
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 137:73254

FILE 'HOME' ENTERED AT 08:20:41 ON 06 APR 2004

Gibbs, T.
10/033243 Page 1
Seq. ID 132

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2004, 21:36:48 ; Search time 2880 Seconds
(without alignments)
316.043 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgtcgaacgttcgagatgat 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	21	6	AX592442	AX592442 Sequence
2	19	90.5	19	6	AX592329	AX592329 Sequence
3	19	90.5	22	6	AX592340	AX592340 Sequence
4	18	85.7	19	6	AX592334	AX592334 Sequence
5	17.8	84.8	164921	8	AF022186	AF022186 Cyanidium
6	17.4	82.9	19	6	AX592366	AX592366 Sequence
7	17.4	82.9	19	6	AX592367	AX592367 Sequence
8	17	81.0	19	6	AX592333	AX592333 Sequence
9	16.8	80.0	658	3	TRE512595	AJ512595 Timarcha
c 10	16.8	80.0	3041	3	AF257638	AF257638 Drosophil
c 11	16.8	80.0	3047	3	AF257637	AF257637 Drosophil
c 12	16.8	80.0	3047	3	AF257639	AF257639 Drosophil
c 13	16.8	80.0	3047	3	AF257640	AF257640 Drosophil
c 14	16.8	80.0	3047	3	AF257641	AF257641 Drosophil
c 15	16.8	80.0	3047	3	AF257643	AF257643 Drosophil
c 16	16.8	80.0	3047	3	AF257646	AF257646 Drosophil
c 17	16.8	80.0	3050	3	AF257642	AF257642 Drosophil
c 18	16.8	80.0	3050	3	AF257644	AF257644 Drosophil
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c 20	16.8	80.0	3050	3	AF257647	AF257647 Drosophil
c 21	16.8	80.0	3050	3	AF257648	AF257648 Drosophil
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c 23	16.8	80.0	146568	2	AC141727	AC141727 Apis mell
24	16.4	78.1	18	6	AX592324	AX592324 Sequence
c 25	16.4	78.1	23	6	BD233619	BD233619 Immunosti
c 26	16.4	78.1	23	6	AR352575	AR352575 Sequence
c 27	16.4	78.1	23	6	AX083677	AX083677 Sequence
c 28	16.4	78.1	23	6	AX148638	AX148638 Sequence
c 29	16.4	78.1	23	6	AX250703	AX250703 Sequence
c 30	16.4	78.1	23	6	AX252293	AX252293 Sequence
c 31	16.4	78.1	23	6	AX252511	AX252511 Sequence
c 32	16.4	78.1	23	6	AX252522	AX252522 Sequence
c 33	16.4	78.1	23	6	AX252936	AX252936 Sequence
c 34	16.4	78.1	23	6	AX253115	AX253115 Sequence
c 35	16.4	78.1	23	6	AX253125	AX253125 Sequence
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c 38	16.4	78.1	73921	8	AB024024	AB024024 Arabidops
c 39	16.2	77.1	1687	8	AK100785	AK100785 Oryza sat
c 40	16.2	77.1	2064	5	AF069993	AF069993 Gallus ga
c 41	16.2	77.1	3135	6	AR346964	AR346964 Sequence
42	16.2	77.1	3960	8	AF152552	AF152552 Sorghum b
c 43	16.2	77.1	3989	4	BTU61233	U61233 Bos taurus
c 44	16.2	77.1	7749	2	AC014752	AC014752 Drosophil
c 45	16.2	77.1	19226	14	CTU56902	U56902 Citrus tris

ALIGNMENTS

RESULT 1
AX592442
LOCUS AX592442 21 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 132 from Patent WO02052002.
ACCESSION AX592442
VERSION AX592442.1 GI:27950544
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 132 04-JUL-2002;
Dynavax Technologies Corporation (US)

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FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             100.0%;  Score 21;  DB 6;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.6;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              |||||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATGAT 21


RESULT 2
AX592329
LOCUS       AX592329                19 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 19 from Patent WO02052002.
ACCESSION   AX592329
VERSION     AX592329.1  GI:27950431
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 19 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             90.5%;  Score 19;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 3
AX592340
LOCUS       AX592340                22 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 30 from Patent WO02052002.
ACCESSION   AX592340
VERSION     AX592340.1  GI:27950442
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 30 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             90.5%;  Score 19;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 8.7;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          4 TCGTCGAACGTTCGAGATG 22


RESULT 4
AX592334
LOCUS       AX592334                19 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 24 from Patent WO02052002.
ACCESSION   AX592334
VERSION     AX592334.1  GI:27950436
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 24 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
     misc_feature    5
                     /note="n = 5-bromocytosine"
ORIGIN

  Query Match             85.7%;  Score 18;  DB 6;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 33;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||| |||||||||||||||
Db          1 TCGTNGAACGTTCGAGATG 19


RESULT 5
AF022186
LOCUS       AF022186              164921 bp    DNA     circular PLN 14-DEC-2000
DEFINITION  Cyanidium caldarium strain RK1 chloroplast, complete genome.
ACCESSION   AF022186 Z36235 Z70297
VERSION     AF022186.2  GI:6466296
KEYWORDS    .
SOURCE      chloroplast Cyanidium caldarium
  ORGANISM  Cyanidium caldarium
            Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales;
            Porphyridiaceae; Cyanidium.
REFERENCE   1  (bases 130696 to 132364)
  AUTHORS   Vogel,H., Fischer,S. and Valentin,K.
  TITLE     A model for the evolution of the plastid sec apparatus inferred
            from secY gene phylogeny
  JOURNAL   Plant Mol. Biol. 32 (4), 685-692 (1996)
  MEDLINE   97134960
   PUBMED   8980520
REFERENCE   2  (bases 1 to 164921)
  AUTHORS   Glockner,G., Rosenthal,A. and Valentin,K.
  TITLE     The structure and gene repertoire of an ancient red algal plastid
            genome
  JOURNAL   J. Mol. Evol. 51 (4), 382-390 (2000)
  MEDLINE   20496959
   PUBMED   11040290
REFERENCE   3  (bases 46857 to 47851)
  AUTHORS   Valentin,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-1996) Institute for Plant Physiology, Justus
            Liebig University, Heinrich Buff Ring 58-62, Giessen 35392, Germany
REFERENCE   4  (bases 28701 to 75580)
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  AUTHORS   Gloeckner,G., Rosenthal,A. and Valentin,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-SEP-1997) Department of Genome Analysis, IMB Jena,
            Beutenbergstr.11, Jena 07745, Germany
REFERENCE   5  (bases 1 to 164921)
  AUTHORS   Gloeckner,G., Rosenthal,A. and Valentin,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1999) Genome Analysis, Institute for Molecular
            Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
REFERENCE   6  (bases 130696 to 132364)
  AUTHORS   Vogel,H., Fischer,S. and Valentin,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1999) Institute for Plant Physiology, Justus
            Liebig University, Heinrich Buff Ring 58-62, Giessen 35392, Germany
COMMENT     On or before Nov 23, 1999 this sequence version replaced gi:529651,
            gi:1240002, gi:2465730.
FEATURES             Location/Qualifiers
     source          1. .164921
                     /organism="Cyanidium caldarium"
                     /organelle="plastid:chloroplast"
                     /mol_type="genomic DNA"
                     /strain="RK1"
                     /db_xref="taxon:2771"
     repeat_region   join(164808. .164921,1. .78,462. .644)
                     /note="direct repeat;
                     repeat unit separated by stem loop"
     stem_loop       339. .477
                     /note="stem-loop separates direct repeat unit"
     rep_origin      580. .780
                     /note="similiar to yeast mitochondrial origin of
                     replication region in GenBank Accession Number L36902"
     gene            986. .2041
                     /gene="psbD"
     mRNA            986. .2041
                     /gene="psbD"
                     /product="unknown"
     CDS             986. .2041
                     /gene="psbD"
                     /note="Photosystem II D2 protein"
                     /codon_start=1
                     /transl_table=11
                     /product="unknown"
                     /protein_id="AAF13026.1"
                     /db_xref="GI:6466445"
                     /translation="MTIAIGREQERGWFDLLDDWLKRDRFVFIGWSGILLFPCAYLAL
                     GAWFTGTTFVSSWYTHGLASSYLEGCNFLTAAVSSPANSMGHSLLFLWGPEAQGDFTR
                     WCQIGGLWTFTALHGSFGLIGFCLRQFEIARLVGLRPYNAIAFSGPIAVFVSVFLLYP
                     LGQASWFFAPSFGVAAIFRFLLFLQGFHNWTLNPFHMMGVAGILGGALLCAIHGATVE
                     NTLFEDGEASDTFRAFTPTQSEETYSMVTANRFWSQIFGVAFANKRWLHFFLLFVPVT
                     GLWVSSIGIVGLALNLRAYDFVSQEIRAAEDPEFETFYTKNILLNEGIRAWMAAQDQP
                     HENFVFPEEVLPRGNAL"
     gene            2031. .3413
                     /gene="psbC"
     mRNA            2031. .3413
                     /gene="psbC"
                     /product="unknown"
     CDS             2031. .3413
                     /gene="psbC"
                     /note="Photosystem II 44 Kd apoprotein"
                     /codon_start=1
                     /transl_table=11
                     /product="unknown"
                     /protein_id="AAF13025.1"
                     /db_xref="GI:6466444"
                     /translation="MLFNKDKNNIGGRSIESTGFAWWSGNARLINLSGKLLGAHVAHA
                     GLIVFWTGAMTLFETSHFIPEKPLYEQGMILLPHLATLGWGVAPGGEIVNTYPYFATG
                     VIHLVSSAVLGFGGIYHSIVGPDVLEDSFSFFGYDWRDKNKMTTILGIHLILLGIGAF
                     LLVIKALFIGGIYDTWAPGGGDIRFITNPTLNPAIIFSYLLKSPFGGEGWIVGVNNME
                     DVIGGHIWIGVTCVIGGIWHILTRPFSWARRAFVWSGEAYLSYSLGALALMGQTAAEY
                     AWYNNTVYPSEFYGPTAAEASQAQAFTFLVRDQRLGANIASTQGPTGLGKYLMRSPTG
                     EVILGGETMRFWDLRAPWLEPLRSSNGLDLNKIKNDIQPWQERRAAEYMTHAPLGSLN
                     SVGGVATEINSVNYVSPRSWLTTSHFFLGFFIFIGHLWHAGRARAAAAGFEKGINREN
                     EPVLSMRPLD"
     gene            3546. .3821
                     /gene="ycf19"
                     /note="similar to ycf19 in Porphyra purpurea"
     mRNA            3546. .3821
                     /gene="ycf19"
                     /product="unknown"
     CDS             3546. .3821
                     /gene="ycf19"
                     /codon_start=1
                     /transl_table=11
                     /product="unknown"
                     /protein_id="AAF13024.1"
                     /db_xref="GI:6466443"
                     /translation="MKDGTDLILETTIAFLQIYIVLILLRMSLGWFPNINWYSQPFYS
                     LSQLSDPYLNLFHGVFPSFLGIDFSPIIGITLIDFIIELLSRQLKPL"
     gene            3873. .4133
                     /gene="ccrf9"
     mRNA            3873. .4133
                     /gene="ccrf9"
                     /product="unknown"
     CDS             3873. .4133
                     /gene="ccrf9"
                     /codon_start=1
                     /transl_table=11
                     /product="unknown"
                     /protein_id="AAF13023.1"
                     /db_xref="GI:6466442"
                     /translation="MNNCLPKNKVFKILNFFKCIDPMCTDNLFKFPLYKLNKNKGKFT
                     NKFYKNTKNKKYIDIWLIFYIYYHIYLRIGKNQTKDLQITKC"
     gene            4189. .4272
                     /gene="ccrf10"
     mRNA            4189. .4272
                     /gene="ccrf10"
                     /product="unknown"
     CDS             4189. .4272
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                     /transl_table=11
                     /product="unknown"
                     /protein_id="AAF13022.1"
                     /db_xref="GI:6466441"
                     /translation="MTKLKSLLNDKKLTLISCLNKTIYDIN"
     tRNA            4334. .4406
                     /product="tRNA-Thr"
     gene            4450. .4971
                     /gene="ycf3"
                     /note="similar to ycf3 in Porphyra purpurea"
     mRNA            4450. .4971
                     /gene="ycf3"
                     /product="unknown"
     CDS             4450. .4971
                     /gene="ycf3"
                     /codon_start=1
                     /transl_table=11
                     /product="unknown"
                     /protein_id="AAF13021.1"
                     /db_xref="GI:6466440"
                     /translation="MPRSQKNDNFIDKTFSIIADLIVKILPTNKESKEAFYYYKDGMA
                     AQSEGEYAEALACYYQALKIEKDPMDKSFILYNIGLIQASNGQHARALEYYHESLKFN
                     PNLVQALNNIAVIYHYYGNKLFEQSKLQEAKLMFDKASNYWRKAIKLAPYNYIEAQNW
                     LKITGRITEDIML"
     gene            5004. .6476
                     /gene="atpB"
     mRNA            5004. .6476
                     /gene="atpB"
                     /product="unknown"
     CDS             5004. .6476
                     /gene="atpB"
                     /note="ATP synthase CF1 beta chain"
                     /codon_start=1
                     /transl_table=11
                     /product="unknown"
                     /protein_id="AAF13020.1"
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                     /db_xref="GI:6466439"
                     /translation="MKPCQLKQKQKTLAIAKVNNKGKVIQIIGPVLDIVFPDGQLPKV
                     FNAIKINNSNNNWITCEVQQLLGDNKVRAVAMSTTEGLKRGASAIDTGEPISIPVGKE
                     TLGRIFNVLGEPIDEKGPVISNDKLPIHRPAPKFTQLETKPSIFETGIKVVDLLAPYR
                     RGGKIGLFGGAGVGKTVLIMELINNVAKAHGGVSVFGGVGERTREGNDLYQEMKESGV
                     INEKDLNLSKVALCYGQMNEPPGARMRVGLTALTMAEYFRDVNKQNVLLFIDNIFRFV
                     QAGSEVSALLGRMPSAVGYQPTLGTEMGALQERITSTLDGSITSIQAVYVPADDLTDP
                     APATTFAHLDATTVLSRALAAKGIYPAVDPLDSTSTMLQPGIVSDEHYTTARKVKETL
                     QRYKELQDIIAILGLDELSEEDRLIVSRARKIEKFLSQPFFVAEVFTGISGKYVSLSD
                     SIKGFNMILSGEVDNIPEQAFYLVGRIEEAIDKAKQVEKS"
     gene            6486. .6887
                     /gene="atpE"
     mRNA            6486. .6887
                     /gene="atpE"
                     /product="unknown"
     CDS             6486. .6887
                     /gene="atpE"
                     /note="ATP synthase CF1 epsilon chain"
                     /codon_start=1
                     /transl_table=11
                     /product="unknown"
                     /protein_id="AAF13019.1"
                     /db_xref="GI:6466438"
                     /translation="MALTVKVITPDRVVWKKTVEEIILPSSTGQLGILMNHAPLLTAL
                     DIGVMRARMVNTWVPLVLLGGFAQIDNNLVTIIVSDAEEVKAIDEEEANKLLAASLAN

  Query Match             84.8%;  Score 17.8;  DB 8;  Length 164921;
  Best Local Similarity   90.5%;  Pred. No. 1.3e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||| | ||||||||||||||||
Db     113659 TCGCCAAACGTTCGAGATGAT 113679


RESULT 6
AX592366
LOCUS       AX592366                 19 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 56 from Patent WO02052002.
ACCESSION   AX592366
VERSION     AX592366.1  GI:27950468
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 56 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             82.9%;  Score 17.4;  DB 6;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 73;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||| ||||||||||||
Db          1 TCGTCGGACGTTCGAGATG 19


RESULT 7
AX592367
LOCUS       AX592367                 19 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 57 from Patent WO02052002.
ACCESSION   AX592367
VERSION     AX592367.1  GI:27950469
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 57 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             82.9%;  Score 17.4;  DB 6;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 73;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||| ||||||||||||
Db          1 TCGTCGTACGTTCGAGATG 19


RESULT 8
AX592333
LOCUS       AX592333                 19 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 23 from Patent WO02052002.
ACCESSION   AX592333
VERSION     AX592333.1  GI:27950435
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 23 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
     misc_feature    2
                     /note="n = 5-bromocytocine"
     misc_feature    5
                     /note="n = 5-bromocytocine"
ORIGIN

  Query Match             81.0%;  Score 17;  DB 6;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              | || ||||||||||||||
Db          1 TNGTNGAACGTTCGAGATG 19


RESULT 9
TRE512595
LOCUS       TRE512595                658 bp    DNA     linear   INV 18-AUG-2003
DEFINITION  Timarcha recticollis 5.8S rRNA gene (partial), 28S rRNA (partial)
            and ITS2, isolate 160.
ACCESSION   AJ512595
VERSION     AJ512595.1  GI:33945511
KEYWORDS    28S ribosomal RNA; 28S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA
            gene; internal transcribed spacer 2; ITS2.
SOURCE      Timarcha recticollis
  ORGANISM  Timarcha recticollis
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            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
            Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
            Timarchini; Timarcha.
REFERENCE   1
  AUTHORS   Gomez-Zurita,J. and Vogler,A.P.
  TITLE     Incongruent nuclear and mitochondrial phylogeographic patterns in
            the Timarcha goettingensis species complex (Coleoptera,
            Chrysomelidae)
  JOURNAL   J. Evol. Biol. 16, 833-843 (2003)
REFERENCE   2  (bases 1 to 658)
  AUTHORS   Gomez-Zurita,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-2002) Gomez-Zurita J., Department of Entomology,
            The Natural History Museum, Cromwell Road, London SW7 5BD, UNITED
            KINGDOM
FEATURES             Location/Qualifiers
     source          1. .658
                     /organism="Timarcha recticollis"
                     /mol_type="genomic DNA"
                     /isolate="16"
                     /db_xref="taxon:79533"
                     /country="Spain:Pla de l'Artiga, Lleida"
     gene            1. .79
                     /gene="5.8S rRNA"
     rRNA            <1. .79
                     /gene="5.8S rRNA"
                     /product="5.8S ribosomal RNA"
     misc_feature    80. .622
                     /note="internal transcribed spacer 2, ITS2"
     gene            623. .658
                     /gene="28S rRNA"
     rRNA            623. .>658
                     /gene="28S rRNA"
                     /product="28S ribosomal RNA"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 658;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              || |||||||||||| |||||
Db        228 CGGCGAACGTTCGAAATGAT 247


RESULT 10
AF257638/c
LOCUS       AF257638               3041 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain CT96_2s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257638
VERSION     AF257638.1  GI:10765243
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3041)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3041)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3041
                     /organism="Drosophila simulans"
                     /mol_type="genomic DNA"
                     /strain="CT96_2s"
                     /db_xref="taxon:7240"
     mRNA            <1. .>1398
                     /product="hexokinase-t1"
     CDS             1. .1398
                     /codon_start=1
                     /product="hexokinase-t1"
                     /protein_id="AAG22945.1"
                     /db_xref="GI:10765244"
                     /translation="MANTFNPEEDFPEVYKVCKLFNPSIDDLEKIKQAMDREITMGLS
                     RDHHDRSTVPCHLSYVQDLPTGRERGQFLALEMMPTNCRIMLVKFSSERDIYTSSKCV
                     IMPHTVAAGRGTEVFTFLATIIANFVKEKKVDKDNLPLGIAFAFTLKKLALDVGILVS
                     WTKEFGAQGAIGKDVVQLLRDALAKFPEISVDVMGIINVGAGSLLALCWAQPDTRIGL
                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
                     SINPGTRIYEKFSGALCMGELVRIIVLRLMKAGAIFAEDRRDYIGIQWKLDMVSLIEI
                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
                     LPQISIAVDGGIYRLHPTFATVLNKYTRLLADPNYNFEFVITQDSCGVGAAIMAGMAH
                     ANKYKTDAKLFTMDY"
     mRNA            join(<1609. .2118,2190. .>3041)
                     /product="hexokinase-t2"
     CDS             join(1609. .2118,2190. .3041)
                     /codon_start=1
                     /product="hexokinase-t2"
                     /protein_id="AAG22946.1"
                     /db_xref="GI:10765245"
                     /translation="MPSLVHTEIETAVKGFLIDQEKMTEVVERMTKEIKMGLAKDTHA
                     RAVIKCFVSHVQDLPTGKERGKYLALDLGGSNFRVLLVNLISNSDVEIMSKGYNFPLT
                     LMSGSGKALFDFLAESLSEFCHTHGLENESLPLGFTFSFPLQQQGLSKGILVAWTKGF
                     SCEGVVGKNVVSLLQEAIDRRGDIKINTVAILNDTVGTLMSCAFYHPNCRIGLIVGTG
                     SNACYVEKTVNAECFEGYQTSPKPSMIINCEWGAFGDNGVLEFVRTSYDKIVDKVTPN
                     PGKQTFEKCISGMYMGELVRLVVIDMIAKGFMFHGIISEKIQERWSFKTAYISDVESD
                     APGEYRNCNKVLSELGILGCQEPDKEALRYICEAVSSRSAKLCACGLVTIINKMNINE
                     VVIGIDGSVYRFHPKYHDMLQYHMKKLLKPGVKFELIVSEDGSGRGAALVAATAVQAK
                     SKL"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3041;
  Best Local Similarity   90.0%;  Pred. No. 3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||| ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 11
AF257637/c
LOCUS       AF257637               3047 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain DPF96_3s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257637
VERSION     AF257637.1  GI:10765240
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3047
                     /organism="Drosophila simulans"
                     /mol_type="genomic DNA"
                     /strain="DPF96_3s"
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     CDS             1. .1398
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                     /db_xref="GI:10765241"
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                     IMPHTVAAGRGTEVFTFLATIIANFVKEKKVDKDNLPLGIAFAFTLKKLALDVGILVS
                     WTKEFGAQGAIGKDVVQLLRDALAKFPEISVDVMGIINVGAGSLLALCWAQPDTRIGL
                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
                     SINPGTRIYEKFSGALCMGELVRIIVLRLMKAGAIFAEDRRDYIGIQWKLDMVSLIEI
                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
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                     ANKYKTDAKLFTMDY"
     mRNA            join(<1615. .2124,2196. .>3047)
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     CDS             join(1615. .2124,2196. .3047)
                     /codon_start=1
                     /product="hexokinase-t2"
                     /protein_id="AAG22944.1"
                     /db_xref="GI:10765242"
                     /translation="MPSLVHTEIETAVKGFLIDQEKMTEVVERMTKEIKMGLAKDTHA
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                     LMSGSGKALFDFLAESLSEFCHTHGLENESLPLGFTFSFPLQQQGLSKGILVAWTKGF
                     SCEGVVGKNVVSLLQEAIDRRGDIKINTVAILNDTVGTLMSCAFYHPNCRIGLIVGTG
                     SNACYVEKTVNAECFEGYQTSPKPSMIINCEWGAFGDNGVLEFVRTSYDKIVDKVTPN
                     PGKQTFEKCISGMYMGELVRLVVIDMIAKGFMFHGIISEKIQERWSFKTAYISDVESD
                     APGEYRNCNKVLSELGILGCQEPDKEALRYICEAVSSRSAKLCACGLVTIINKMNINE
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                     SKL"

ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3047;
  Best Local Similarity   90.0%;  Pred. No. 3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
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Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 12
AF257639/c
LOCUS       AF257639                3047 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain CT96_5s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257639
VERSION     AF257639.1  GI:10765246
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3047
                     /organism="Drosophila simulans"
                     /mol_type="genomic DNA"
                     /strain="CT96_5s"
                     /db_xref="taxon:7240"
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     CDS             1. .1398
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                     /product="hexokinase-t1"
                     /protein_id="AAG22947.1"
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                     IMPHTVAAGRGTEVFTFLATIIANFVKEKKVDKDNLPLGIAFAFTLKKLALDVGILVS
                     WTKEFGAQGAIGKDVVQLLRDALAKFPEISVDVMGIINVGAGSLLALCWAQPDTRIGL
                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
                     SINPGTRIYEKFSGALCMGELVRIIVLRLMKAGAIFAEDRRDYIGIQWKLDMVSLIEI
                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
                     LPQISIAVDGGIYRLHPTFATVLNKYTRLLADPNYNFEFVITQDSCGVGAAIMAGMAH
                     ANKYKTDAKLFTMDY"
     mRNA            join(<1615. .2124,2196. .>3047)
                     /product="hexokinase-t2"
     CDS             join(1615. .2124,2196. .3047)
                     /codon_start=1
                     /product="hexokinase-t2"
                     /protein_id="AAG22948.1"
                     /db_xref="GI:10765248"
                     /translation="MPSLVHTEIETAVKGFLIDQEKMTEVVERMTKEIKMGLAKDTHA
                     RAVIKCFVSHVQDLPTGKERGKYLALDLGGSNFRVLLVNLISNSDVEIMSKGYNFPLT
                     LMSGSGKALFDFLAESLSEFCHTHGLENESLPLGFTFSFPLQQQGLSKGILVAWTKGF
                     SCEGVVGKNVVSLLQEAIDRRGDIKINTVAILNDTVGTLMSCAFYHPNCRIGLIVGTG
                     SNACYVEKTVNAECFEGYQTSPKPSMIINCEWGAFGDNGVLEFVRTSYDKIVDKVTPN
                     PGKQTFEKCISGMYMGELVRLVVIDMIAKGFMFHGIISEKIQERWSFKTAYISDVESD
                     APGEYRNCNKVLSELGILGCQEPDKEALRYICEAVSSRSAKLCACGLVTIINKMNINE
                     VVIGIDGSVYRFHPKYHDMLQYHMKKLLKPGVKFELIVSEDGSGRGAALVAATAVQAK
                     SKL"

ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3047;
  Best Local Similarity   90.0%;  Pred. No. 3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              |||||||||| ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 13
AF257640/c
LOCUS       AF257640                3047 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain CT96_6s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257640
VERSION     AF257640.1  GI:10765249
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3047
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                     /db_xref="taxon:7240"
     mRNA            <1. .>1398
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                     IMPHTVAAGRGTEVFTFLATIIANFVKEKKVDKDNLPLGIAFAFTLKKLALDVGILVS
                     WTKEFGAQGAIGKDVVQLLRDALAKFPEISVDVMGIINVGAGSLLALCWAQPDTRIGL
                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
                     SINPGTRIYEKFSGALCMGELVRIIVLRLMKAGAIFAEDRRDYIGIQWKLDMVSLIEI
                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
                     LPQISIAVDGGIYRLHPTFATVLNKYTRLLADPNYNFEFVITQDSCGVGAAIMAGMAH
                     ANKYKTDAKLFTMDY"
     mRNA            join(<1615. .2124,2196. .>3047)
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     CDS             join(1615. .2124,2196. .3047)
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                     SCEGVVGKNVVSLLQEAIDRRGDIKINTVAILNDTVGTLMSCAFYHPNCRIGLIVGTG
                     SNACYVEKTVNAECFEGYQTSPKPSMIINCEWGAFGDNGVLEFVRTSYDKIVDKVTPN
                     PGKQTFEKCISGMYMGELVRLVVIDMIAKGFMFHGIISEKIQERWSFKTAYISDVESD
                     APGEYRNCNKVLSELGILGCQEPDKEALRYICEAVSSRSAKLCACGLVTIINKMNINE
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                     SKL"
ORIGIN

  Query Match           80.0%;  Score 16.8;  DB 3;  Length 3047;
  Best Local Similarity  90.0%;  Pred. No. 3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||| ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 14
AF257641/c
LOCUS       AF257641               3047 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain VA96_5s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257641
VERSION     AF257641.1  GI:10765252
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3047
                     /organism="Drosophila simulans"
                     /mol_type="genomic DNA"
                     /strain="VA96_5s"
                     /db_xref="taxon:7240"
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     CDS             1. .1398
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                     /product="hexokinase-t1"
                     /protein_id="AAG22951.1"
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                     IMPHTVAAGRGTEVFTFLATIIANFVKEKKVDKDNLPLGIAFAFTLKKLALDVGILVS
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                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
                     SINPGTRIYEKFSGALCMGELVRIIVLRLMKAGAIFAEDRRDYIGIQWKLDMVSLIEI
                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
                     LPQISIAVDGGIYRLHPTFATVLNKYTRLLADPNYNFEFVITQDSCGVGAAIMAGMAH
                     ANKYKTDAKLFTMDY"
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                     SNACYVEKTVNAECFEGYQTSPKPSMIINCEWGAFGDNGVLEFVRTSYDKIVDKVTPN
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                     SKL"
ORIGIN

  Query Match           80.0%;  Score 16.8;  DB 3;  Length 3047;
  Best Local Similarity  90.0%;  Pred. No. 3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||| ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 15
AF257643/c
LOCUS       AF257643               3047 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain VA96_8s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257643
VERSION     AF257643.1  GI:10765258
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3047
                     /organism="Drosophila simulans"
                     /mol_type="genomic DNA"
                     /strain="VA96_8s"
                     /db_xref="taxon:7240"
     mRNA            <1. .>1398
                     /product="hexokinase-t1"
     CDS             1. .1398
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                     IMPHTVAAGRGTEVFTFLATIIANFVKEKKVDKDNLPLGIAFAFTLKKLALDVGILVS
                     WTKEFGAQGAIGKDVVQLLRDALAKFPEISVDVMGIINVGAGSLLALCWAQPDTRIGL
                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
                     SINPGTRIYEKFSGALCMGELVRIIVLRLMKAGAIFAEDRRDYIGIQWKLDMVSLIEI
                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
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     mRNA            join(<1615. .2124,2196. .>3047)
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                     SNACYVEKTVNAECFEGYQTSPKPSMIINCEWGAFGDNGVLEFVRTSYDKIVDKVTPN
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                     SKL"

ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3047;
  Best Local Similarity   90.0%;  Pred. No. 3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||| ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 16
AF257646/c
LOCUS       AF257646               3047 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain GA96_5s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257646
VERSION     AF257646.1  GI:10765267
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3047)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3047
                     /organism="Drosophila simulans"
                     /mol_type="genomic DNA"
                     /strain="GA96_5s"
                     /db_xref="taxon:7240"
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     CDS             1. .1398
                     /codon_start=1
                     /product="hexokinase-t1"
                     /protein_id="AAG22961.1"
                     /db_xref="GI:10765268"
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                     IMPHTVAAGRGTEVFTFLATIIANFVKEKKVDKDNLPLGIAFAFTLKKLALDVGILVS
                     WTKEFGAQGAIGKDVVQLLRDALAKFPEISVDVMGIINVGAGSLLALCWAQPDTRIGL
                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
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                     SCEGVVGKNVVSLLQEAIDRRGDIKINTVAILNDTVGTLMSCAFYHPNCRIGLIVGTG
                     SNACYVEKTVNAECFEGYQTSPKPSMIINCEWGAFGDNGVLEFVRTSYDKIVDKVTPN
                     PGKQTFEKCISGMYMGELVRLVVIDMIAKGFMFHGIISEKIQERWSFKTAYISDVESD
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                     SKL"

ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3047;
  Best Local Similarity   90.0%;  Pred. No. 3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||| ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 17
AF257642/c
LOCUS       AF257642               3050 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain VA96_7s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257642
VERSION     AF257642.1  GI:10765255
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3050)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3050)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3050
                     /organism="Drosophila simulans"
                     /mol_type="genomic DNA"
                     /strain="VA96_7s"
                     /db_xref="taxon:7240"
     mRNA            <1. .>1398
                     /product="hexokinase-t1"
     CDS             1. .1398
                     /codon_start=1
                     /product="hexokinase-t1"
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                     IMPHTVAAGRGTEVFTFLATIIANFVKEKKVDKDNLPLGIAFAFTLKKLALDVGILVS
                     WTKEFGAQGAIGKDVVQLLRDALAKFPEISVDVMGIINVGAGSLLALCWAQPDTRIGL
                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
                     SINPGTRIYEKFSGALCMGELVRIIVLRLMKAGAIFAEDRRDYIGIQWKLDMVSLIEI
                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
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     mRNA            join(<1618. .2127,2199. .>3050)
                     /product="hexokinase-t2"
     CDS             join(1618. .2127,2199. .3050)
                     /codon_start=1
                     /product="hexokinase-t2"
                     /protein_id="AAG22954.1"
                     /db_xref="GI:10765257"
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                     SCEGVVGKNVVTLLQEAIDRRGDIKINTVAILNDTVGTLMSCAFYHPNCRIGLIVGTG
                     SNACYVEKTVNAECFEGYQTSPKPSMIINCEWGAFGDNGVLEFVRTSYDKIVDKVTPN
                     PGKQTFEKCISGMYMGELVRLVVIDMIAKGFMFHGIISEKIQERWSFKTAYISDVESD
                     APGEYRNCNKVLSELGILGCQEPDKEALRYICEAVSSRSAKLCACGLVTIINKMNINE
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                     SKL"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3050;
  Best Local Similarity   90.0%;  Pred. No. 3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||| ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 18
AF257644/c
LOCUS       AF257644               3050 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain GA96_2s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257644
VERSION     AF257644.1  GI:10765261
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3050)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3050)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3050
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                     /mol_type="genomic DNA"
                     /strain="GA96_2s"
                     /db_xref="taxon:7240"
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     CDS             1. .1398
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                     /protein_id="AAG22957.1"
                     /db_xref="GI:10765262"
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                     IMPHTVAAGRGTEVFTFLATIIANFVKEKKVDKDNLPLGIAFAFTLKKLALDVGILVS
                     WTKEFGAQGAIGKDVVQLLRDALAKFPEISVDVMGIINVGAGSLLALCWAQPDTRIGL
                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
                     SINPGTRIYEKFSGALCMGELVRIIVLRLMKAGAIFAEDRRDYIGIQWKLDMVSLIEI
                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
                     LPQISIAVDGGIYRLHPTFATVLNKYTRLLADPNYNFEFVITQDSCGVGAAIMAGMAH
                     ANKYKTDAKLFTMDY"
     mRNA            join(<1618. .2127,2199. .>3050)
                     /product="hexokinase-t2"
     CDS             join(1618. .2127,2199. .3050)
                     /codon_start=1
                     /product="hexokinase-t2"
                     /protein_id="AAG22958.1"
                     /db_xref="GI:10765263"
                     /translation="MPSLVHTEIETAVKGFLIDQEKMTEVVERMTKEIKMGLAKDTHA
                     RAVIKCFVSHVQDLPTGKERGKYLALDLGGSNFRVLLVNLISSSDVEIMSKGYNFPLT
                     LMSGSGKALFDFLAESLSEFCHTHGLENESLPLGFTFSFPLQQQGLSKGILVAWTKGF
                     SCEGVVGKNVVTLLQEAIDRRGDIKINTVAILNDTVGTLMSCAFYHPNCRIGLIVGTG
                     SNACYVEKTVNAECFEGYQTSPKPSMIINCEWGAFGDNGVLEFVRTSYDKIVDKVTPN
                     PGKQTFEKCISGMYMGELVRLVVIDMIAKGFMFHGIISEKIQERWSFKTAYISDVESD
                     APGEYRNCNKVLSELGILGCQEPDKEALRYICEAVSSRSAKLCACGLVTIINKMNINE
                     VVIGIDGSVYRFHPKYHDMLQYHMKKLLKPGVKFELIVSEDGSGRGAALVAATAVQAK
                     SKL"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3050;
  Best Local Similarity   90.0%;  Pred. No. 3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||| ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 19
AF257645/c
LOCUS       AF257645               3050 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain GA96_4s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257645
VERSION     AF257645.1  GI:10765264
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3050)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3050)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3050
                     /organism="Drosophila simulans"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:7240"
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     CDS             1. .1398
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                     /protein_id="AAG22959.1"
                     /db_xref="GI:10765265"
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                     WTKEFGAQGAIGKDVVQLLRDALAKFPEISVDVMGIINVGAGSLLALCWAQPDTRIGL
                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
                     SINPGTRIYEKFSGALCMGELVRIIVLRLMKAGAIFAEDRRDYIGIQWKLDMVSLIEI
                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
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     mRNA            join(<1618. .2127,2199. .>3050)
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                     /protein_id="AAG22960.1"
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                     SCEGVVGKNVVTLLQEAIDRRGDIKINTVAILNDTVGTLMSCAFYHPNCRIGLIVGTG
                     SNACYVEKTVNAECFEGYQTSPKPSMIINCEWGAFGDNGVLEFVRTSYDKIVDKVTPN
                     PGKQTFEKCISGMYMGELVRLVVIDMIAKGFMFHGIISEKIQERWSFKTAYISDVESD
                     APGEYRNCNKVLSELGILGCQEPDKEALRYICEAVSSRSAKLCACGLVTIINKMNINE
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                     SKL"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3050;
  Best Local Similarity   90.0%;  Pred. No. 3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||| ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 20
AF257647/c
LOCUS       AF257647               3050 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain HFL97_1s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257647
VERSION     AF257647.1  GI:10765270
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3050)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3050)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3050
                     /organism="Drosophila simulans"
                     /mol_type="genomic DNA"
                     /strain="HFL97_1s"
                     /db_xref="taxon:7240"
     mRNA            <1. .>1398
                     /product="hexokinase-t1"
     CDS             1. .1398
                     /codon_start=1
                     /product="hexokinase-t1"
                     /protein_id="AAG22963.1"
                     /db_xref="GI:10765271"
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                     IMPHTVAAGRGTEVFTFLATIIANFVKEKKVDKDNLPLGIAFAFTLKKLALDVGILVS
                     WTKEFGAQGAIGKDVVQLLRDALAKFPEISVDVMGIINVGAGSLLALCWAQPDTRIGL
                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
                     SINPGTRIYEKFSGALCMGELVRIIVLRLMKAGAIFAEDRRDYIGIQWKLDMVSLIEI
                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
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                     ANKYKTDAKLFTMDY"
     mRNA            join(<1618. .2127,2199. .>3050)
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                     PGKQTFEKCISGMYMGELVRLVVIDMIAKGFMFHGIISEKIQERWSFKTAYISDVESD
                     APGEYRNCNKVLSELGILGCQEPDKEALRYICEAVSSRSAKLCACGLVTIINKMNINE
                     VVIGIDGSVYRFHPKYHDMLQHHMKKLLKPGVKFELIVSEDGSGRGAALVAATAVQAK
                     SKL"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3050;
  Best Local Similarity   90.0%;  Pred. No. 3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||| ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 21
AF257648/c
LOCUS       AF257648               3050 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain HFL97_2s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257648
VERSION     AF257648.1  GI:10765273
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3050)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3050)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3050
                     /organism="Drosophila simulans"
                     /mol_type="genomic DNA"
                     /strain="HFL97_2s"
                     /db_xref="taxon:7240"
     mRNA            <1. .>1398
                     /product="hexokinase-t1"
     CDS             1. .1398
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                     /product="hexokinase-t1"
                     /protein_id="AAG22965.1"
                     /db_xref="GI:10765274"
                     /translation="MANTFNPEEDFPEVYKVCKLFNPSIDDLEKIKQAMDREITMGLS
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                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
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                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
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                     SKL"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3050;
  Best Local Similarity   90.0%;  Pred. No. 3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              |||||||||  ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 22
AF257649/c
LOCUS       AF257649               3050 bp    DNA     linear   INV 09-OCT-2000
DEFINITION  Drosophila simulans strain HFL97_4s hexokinase-t1 and hexokinase-t2
            genes, complete cds.
ACCESSION   AF257649
VERSION     AF257649.1  GI:10765276
KEYWORDS    .
SOURCE      Drosophila simulans
  ORGANISM  Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3050)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Contrasting molecular population genetics of four hexokinases in
            Drosophila melanogaster and Drosophila simulans
  JOURNAL   Genetics (2000) In press
REFERENCE   2  (bases 1 to 3050)
  AUTHORS   Duvernell,D.D. and Eanes,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-2000) Ecology and Evolution, State University of
            New York, Stony Brook, NY 11794, USA
FEATURES             Location/Qualifiers
     source          1. .3050
                     /organism="Drosophila simulans"
                     /mol_type="genomic DNA"
                     /strain="HFL97_4s"
                     /db_xref="taxon:7240"
     mRNA            <1. .>1398
                     /product="hexokinase-t1"
     CDS             1. .1398
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                     /product="hexokinase-t1"
                     /protein_id="AAG22967.1"
                     /db_xref="GI:10765277"
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                     WTKEFGAQGAIGKDVVQLLRDALAKFPEISVDVMGIINVGAGSLLALCWAQPDTRIGL
                     IMGSIANSCYVERVERCETYEGDEFRRLMIINSDWAHFGDTGQLDFIRNEFDRLLDTD
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                     VSDPPGVYTKAQEVMDKFRIRHCKERDLAALKYICDTVTNRAAMLVASGVSCLIDRMR
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     mRNA            join(<1618. .2127,2199. .>3050)
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                     SCEGVVGKNVVTLLQEAIDRRGDIKINTVAILNDTVGTLMSCAFYHPNCRIGLIVGTG
                     SNACYVEKTVNAECFEGYQTSPKPSMIINCEWGAFGDNGVLEFVRTSYDKIVDKVTPN
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                     SKL"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 3;  Length 3050;
  Best Local Similarity   90.0%;  Pred. No. 3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              |||||||||  ||| ||||||
Db        156 CGTCGAACGATCGTGATGAT 137


RESULT 23
AC141727/c
LOCUS       AC141727               146568 bp    DNA     linear   HTG 19-MAR-2003
DEFINITION  Apis mellifera clone CH224-57G3, WORKING DRAFT SEQUENCE, 25
            unordered pieces.
ACCESSION   AC141727
VERSION     AC141727.1  GI:29123911
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Apis mellifera (honeybee)
  ORGANISM  Apis mellifera
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
            Apidae; Apis.
REFERENCE   1  (bases 1 to 146568)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
            Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
            Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
            Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
            Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
            Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
            Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
            Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
            Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
            Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
            Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
            Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
            Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
            Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
            Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
            Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
            Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
            Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
            Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
            Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
            Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
            Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
            Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
            Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
            Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
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            Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
            Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
            Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
            Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
            Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
            Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
            Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
            Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
            Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
            Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
            Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
            Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
            Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 146568)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: AMEZ
                Center clone name: CH224-57G3
            -------------- Summary Statistics
                Sequencing vector: Plasmid;
                Chemistry: Dye-terminator Big Dye: 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 132495 bases at least Q40
                Consensus quality: 137202 bases at least Q30
                Consensus quality: 140042 bases at least Q20
                Estimated insert size: 137866; sum-of-contigs estimation
                Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 25 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1456: contig of 1456 bp in length
            *     1457     1556: gap of unknown length
            *     1557     2731: contig of 1175 bp in length
            *     2732     2831: gap of unknown length
            *     2832     4180: contig of 1349 bp in length
            *     4181     4280: gap of unknown length
            *     4281     5835: contig of 1555 bp in length
            *     5836     5935: gap of unknown length
            *     5936     7358: contig of 1423 bp in length
            *     7359     7458: gap of unknown length
            *     7459     8816: contig of 1358 bp in length
            *     8817     8916: gap of unknown length
            *     8917    10936: contig of 2020 bp in length
            *    10937    11036: gap of unknown length
            *    11037    12381: contig of 1345 bp in length
            *    12382    12481: gap of unknown length
            *    12482    15062: contig of 2581 bp in length
            *    15063    15162: gap of unknown length
            *    15163    18933: contig of 3771 bp in length
            *    18934    19033: gap of unknown length
            *    19034    23106: contig of 4073 bp in length
            *    23107    23206: gap of unknown length
            *    23207    27707: contig of 4501 bp in length
            *    27708    27807: gap of unknown length
            *    27808    33059: contig of 5252 bp in length
            *    33060    33159: gap of unknown length
            *    33160    38669: contig of 5510 bp in length
            *    38670    38769: gap of unknown length
            *    38770    45436: contig of 6667 bp in length
            *    45437    45536: gap of unknown length
            *    45537    52247: contig of 6711 bp in length
            *    52248    52347: gap of unknown length
            *    52348    59244: contig of 6897 bp in length
            *    59245    59344: gap of unknown length
            *    59345    66497: contig of 7153 bp in length
            *    66498    66597: gap of unknown length
            *    66598    74127: contig of 7530 bp in length
            *    74128    74227: gap of unknown length
            *    74228    81722: contig of 7495 bp in length
            *    81723    81822: gap of unknown length
            *    81823    92875: contig of 11053 bp in length
            *    92876    92975: gap of unknown length
            *    92976   101243: contig of 8268 bp in length
            *   101244   101343: gap of unknown length
            *   101344   113869: contig of 12526 bp in length
            *   113870   113969: gap of unknown length
            *   113970   128447: contig of 14478 bp in length
            *   128448   128547: gap of unknown length
            *   128548   146568: contig of 18021 bp in length.
FEATURES             Location/Qualifiers
     source          1. .146568
                     /organism="Apis mellifera"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7460"
                     /clone="CH224-57G3"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 2;  Length 146568;
  Best Local Similarity   90.0%;  Pred. No. 4.7e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              |||||||||||||||| | |
Db     135270 CGTCGAACGTTCGAGACGTT 135251


RESULT 24
AX592324
LOCUS       AX592324                 18 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 14 from Patent WO02052002.
ACCESSION   AX592324
VERSION     AX592324.1  GI:27950426
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 14 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 6;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATG 19
              | ||||||||||||||||
Db          1 CTTCGAACGTTCGAGATG 18
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RESULT 25
BD233619/c
LOCUS       BD233619                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Immunostimulatory oligonucleotides, compositions thereof and
            methods of use thereof.
ACCESSION   BD233619
VERSION     BD233619.1  GI:33043389
KEYWORDS    JP 2002517156-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Schwartz,D., Roman,M., Dina,D. and Raz,E.
  TITLE     Immunostimulatory oligonucleotides, compositions thereof and
            methods of use thereof
  JOURNAL   Patent: JP 2002517156-A 4 11-JUN-2002;
            DYNAVAX TECHNOLOGIES CORP
COMMENT     OS   Unidentified
            PN   JP 2002517156-A/4
            PD   11-JUN-2002
            PF   05-JUN-1998 JP 1999502884
            PR   06-JUN-1997 US    60/048793
            PI   DAVID SCHWARTZ,MARK ROMAN,DINO DINA,EYAL RAZ
            PC
            C12N15/09,A61K31/7088,A61K31/7115,A61P37/02,A61P43/00,C12Q1/68, PC
             C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Immunostimulatory oligonucleotides, compositions thereof and
            CC            methods of
            CC   use thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 6;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 26
AR352575/c
LOCUS       AR352575                  23 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 4 from patent US 6589940.
ACCESSION   AR352575
VERSION     AR352575.1  GI:33757826
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Raz,E., Roman,M. and Dina,D.
  TITLE     Immunostimulatory oligonucleotides, compositions thereof and
            methods of use thereof
  JOURNAL   Patent: US 6589940-A 4 08-JUL-2003;
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 6;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 27
AX083677/c
LOCUS       AX083677                  23 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 3 from Patent WO0112223.
ACCESSION   AX083677
VERSION     AX083677.1  GI:13185409
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of modulating an immune response using immunostimulatory s
            equences and compositions for use therein
  JOURNAL   Patent: WO 0112223-A 3 22-FEB-2001;
            Dynavax Technologies Corporation (US)
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Synthetic construct"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 6;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 28
AX148638/c
LOCUS       AX148638                  23 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 3 from Patent WO0135991.
ACCESSION   AX148638
VERSION     AX148638.1  GI:14347256
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tuck,S. and van Nest,G.
  TITLE     Immunomodulatory compositions containing an immunostimulatory
            sequence linked to antigen and methods of use thereof
  JOURNAL   Patent: WO 0135991-A 3 25-MAY-2001;
            Dynavax Technologies Corporation (US)
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="synthetic construct"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 6;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1
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RESULT 29
AX250703/c
LOCUS       AX250703                  23 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 3 from Patent WO0168078.
ACCESSION   AX250703
VERSION     AX250703.1  GI:15984441
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of suppressing hepatitis virus infection using
            immunomodulatory polynucleotide sequences
  JOURNAL   Patent: WO 0168078-A 3 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 6;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 30
AX252293/c
LOCUS       AX252293                  23 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 3 from Patent WO0168117.
ACCESSION   AX252293
VERSION     AX252293.1  GI:15985634
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of reducing papillomavirus infection using immunomodulatory
            polynucleotide sequences
  JOURNAL   Patent: WO 0168117-A 3 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 6;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 31
AX252511/c
LOCUS       AX252511                  23 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 3 from Patent WO0168103.
ACCESSION   AX252511
VERSION     AX252511.1  GI:15985782
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of ameliorating symptoms of herpes infection using
            immunoodulatory polynucleotide sequences
  JOURNAL   Patent: WO 0168103-A 3 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 6;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 32
AX252522/c
LOCUS       AX252522                  23 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 3 from Patent WO0168144.
ACCESSION   AX252522
VERSION     AX252522.1  GI:15985793
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G. and Tuck,S.
  TITLE     Biodegradable immunomodulatory formulations and methods for use
            thereof
  JOURNAL   Patent: WO 0168144-A 3 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 6;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 33
AX252936/c
LOCUS       AX252936                  23 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 3 from Patent WO0168143.
ACCESSION   AX252936
VERSION     AX252936.1  GI:15986203
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G. and Tuck,S.
  TITLE     Immunomodulatory formulations and methods for use thereof
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  JOURNAL   Patent: WO 0168143-A 3 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 6;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || ||||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 34
AX253115/c
LOCUS       AX253115                  23 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 3 from Patent WO0168116.
ACCESSION   AX253115
VERSION     AX253115.1  GI:15986283
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of preventing and treating respiratory viral infeciton usi
            ng immunomodulatory polynucleotide sequences
  JOURNAL   Patent: WO 0168116-A 3 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 6;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || ||||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 35
AX253125/c
LOCUS       AX253125                  23 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 3 from Patent WO0168077.
ACCESSION   AX253125
VERSION     AX253125.1  GI:15986293
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Nest,G.
  TITLE     Methods of preventing and treating viral infections using
            immunodulatory polynucleotide sequences
  JOURNAL   Patent: WO 0168077-A 3 20-SEP-2001;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 6;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || ||||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 36
ATH528591
LOCUS       ATH528591                 416 bp    DNA     linear   PLN 29-MAR-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            168C08.
ACCESSION   AJ528591
VERSION     AJ528591.1  GI:26796851
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 416)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:3702"
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     misc_feature    1. .416
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 8;  Length 416;
  Best Local Similarity   94.4%;  Pred. No. 4e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATGAT 21
              |||||| ||||||||||
Db        155 TCGAACGGTCGAGATGAT 172


RESULT 37
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AC005310
LOCUS       AC005310               68415 bp    DNA     linear   PLN 27-FEB-2002
DEFINITION  Arabidopsis thaliana chromosome 2 clone F19D11 map CIC06C03,
            complete sequence.
ACCESSION   AC005310
VERSION     AC005310.3  GI:20197315
KEYWORDS    HTG.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 68415)
  AUTHORS   Rounsley,S.D., Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Mason,T.M.,
            Shen,M., Ronning,C.M., Fraser,C.M., Somerville,C.R. and Venter,J.C.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 68415)
  AUTHORS   Lin,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
            Medical Center Dr., Rockville, MD 20850, USA
REFERENCE   3  (bases 1 to 68415)
  AUTHORS   Town,C.D. and Kaul,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
COMMENT     On Apr 18, 2002 this sequence version replaced gi:6598455.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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                     /map="CIC06C03"
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                     /note="overlap with BAC clone T3A4
                     (AC005819:55355. .55870)."
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                     /note="synonym: F19D11.1; predicted by genscan"
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     gene            3626. .4289
                     /gene="At2g46735"
                     /note="synonym: F19D11.26; supported by full length cDNA:
                     Ceres: 105240"
     mRNA            3626. .4289
                     /gene="At2g46735"
     CDS             3684. .4166
                     /gene="At2g46735"
                     /codon_start=1
                     /product="Expressed protein"
                     /protein_id="AAM15019.1"
                     /db_xref="GI:20197318"
                     /translation="MWTVKPAAMPVQFHMRPTVATSVAYSQPPPHNYDGIHRRFINVP
                     TKSQTSESVGGLGQQILLRTVDSNPRKPIPKETEISGSDVLWAIQRATAQRKRTNAGK
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                     5963. .>6664))
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                     WGVTVGGMMGTGAHGSSLWGKGSAVHDYVTEIRMVSPGSVNDGFAKIRVLSETTTPNE
                     FNAAKVSLGVLGVISQVTFELQPMFKRSLKYVMRNDLDFNDEALTFGKKHEFADFVWL
                     PSQGKVVYRMDDRVAVNTLGNGLYDFFPFRSQLSAVLATTRSSEETQETLRDAHGKCV
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                     /note="synonym: F19D11.3"
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                     TAMTMTVESGMTLRQLIVEAAKVGLALPYAPYWWGLTVGGMMGTGAHGSSLWGKGSAV
                     HDYVTEIRMVSPGSVNEGFAKIRILSETTTPNEFNAAKVSLGVLGVISQVTFELQPMF
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                     FLPFRSQLSAAIAIIRTSEETQERFRDANGKCVGATIISSTLFAPSYGLTNNGIIFTG
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     repeat_region   11813. .11836
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                     /gene="At2g46760"
                     /note="synonym: F19D11.4"
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                     TPKEFNAAKVSLGVLGVISQVTLKLQPMFKRSLRYVMRNDSDFGDQAVTFGMKHEFAD
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     repeat_region   15764. .15791
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     repeat_region   15978. .16009
                     /rpt_family="AT_rich"
     repeat_region   complement(16139. .16202)
                     /rpt_family="(TA)n"
     repeat_region   complement(18735. .18755)
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  Query Match             78.1%;  Score 16.4;  DB 8;  Length 68415;
  Best Local Similarity   94.4%;  Pred. No. 7.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATGAT 21
              |||| ||||||||||||
Db      23461 TCGATCGTTCGAGATGAT 23478


RESULT 38
AB024024/c
LOCUS       AB024024               73921 bp    DNA     linear   PLN 27-DEC-2000
DEFINITION  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K15C23.
ACCESSION   AB024024 BA000015
VERSION     AB024024.1  GI:4519183
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (sites)
  AUTHORS   Kaneko,T., Katoh,T., Asamizu,E., Sato,S., Nakamura,Y., Kotani,H.
            and Tabata,S.
  TITLE     Structural analysis of Arabidopsis thaliana chromosome 5. XI
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 73921)
  AUTHORS   Nakamura,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-1999) Yasukazu Nakamura, Kazusa DNA Research
            Institute, Department of Plant Gene Research; 1532-3, Yana,
            Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
            Tel:81-438-52-3935, Fax:81-438-52-3934)
COMMENT     Address for correspondence: kaos@kazusa.or.jp
            For the latest information on annotation of this clone, please see
            http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=K15C23
            Genes with similarity to proteins in the databases are described in
            'product' or 'note' qualifiers.  Genes that have no significant
            protein similarity are described as 'unknown protein'.
            The software programs used to predict genes include: Grail
            (Informatics Group, Oak Ridge National Laboratory,
            http://compbio.ornl.gov/Grail-1.3/),
            GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
            NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
            Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
            SplicePredictor (Volker Brendel, Stanford University,
            http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
            Genes encoding tRNAs are predicted by tRNAscan-SE
            (Sean Eddy, Washington University School of Medicine, St. Louis,
            http://genome.wustl.edu/eddy/tRNAscan-SE/).
            This sequence may not be the entire insert of this clone. It may be
            shorter because we remove overlaps between neighboring submissions.
            The 5' clone is MFC16 and the 3' clone is K23L20.
FEATURES                Location/Qualifiers
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                        RSSIQSTDAACAAATTTAPAPDAECSHTSPNAAVVTTAAENACIITAATNALSTSFVA
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     CDS                join(31482. .31599,31784. .31867,32242. .32336)
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                        /protein_id="BAA98111.1"
                        /db_xref="GI:8953756"
                        /translation="MERKKFSSKFIHLLIVFLLLCTFLSRTESALPYHHELFLGRKRM
                        NYYKPNSAIGTPSSTSDHAPGSNGRKLMSIYRPNGDIFTGPSGSGHGGGRTPAP"
     CDS                join(39746. .40013,40093. .40148,40217. .40330,40438. .40515,
                        40605. .40734,40814. .40866,40945. .41118,41206. .41382)
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VDLFADGKVLDQLQEIPMWLELASRLMPNGRLMVNCAGIETEVKNGKPELVLDDLAWM
LNSTVKILSEAFPGQVSWKRTPDSEGLNFVALTGGLPDLSDWSSKVPVRLSESVKLWK
LCETVPLQLGALNAS"

CDS join(42022. .42331,42450. .42478,42633. .42692,42768. .42845,
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CDS complement(45873. .46379)
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CDS complement(join(50063. .50683,50756. .51694))
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CDS join(55435. .55539,55654. .55938,56038. .56420,56505. .56726,
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PDYMENLQGHMKTAFKFVMYLFKEYEEILRSQGRSFVLEKMIEEWARGGHVPSFDEYI
ESGGAEIGTYATIACSIMGLGEIGKKEAFEWLISRPKLVRILGAKTRLMDDIADFEED
MEKGYTANALNYYMNEHGVTKEEASRELEKMNGDMNKIVNEECLKITTMPRRILMQSV
NYARSLDVLYTADDVYNHREGKLKEYMRLLLVDPILL"

CDS complement(join(58589. .58741,58812. .58942,59021. .59131,
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61131. .61205,61289. .61484,61588. .61781,61890. .62052,
62160. .62285,62387. .62539,62621. .62697))
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/pseudo
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/evidence=not_experimental
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CDS 63301. .64824
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SYDFIGINYYSSSYAKDVPCSSENVTLFSDPCASVTGEREGVPIGPKAASDWLLIYPK
GIRDLLLYAKYKFKDPVMYITENGRDEASTGKIDLKDSERIDYYAQHLKMVQDAISIG
ANVKGFFAWSLLDNFEWATGYSVRFGLVYVDFNDGRKRYPKKSAKWFRKLLSEKKRN"

CDS join(65551. .65895,65972. .66016,66102. .66215,66686. .66766,
67046. .67213,67358. .67447)
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/evidence=not_experimental
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DPEDLKYVNEIKRVIELLRRNRDMIFSEVKLTIMIEDPRELERRRLLGIEDADTPSRD
DLAEALEQVNDGKIPKDRATLRMLHEEMIRWPNLEVEVSKKQRGKSMYAKSTDTGIDP
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NSLQ"

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/db_xref="GI:8953764"
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RSGLMRALRNREQDSLPNSPKQRSGLMRAFRNKDQDSLPNSTTGSPKQRSGLMRALRN
KEQDSLPNSTTGSPKQRSGLMRALRNKEQDSSSASYKRSKSCGSTSKTLSHKSSGIRN

Query Match 78.1%; Score 16.4; DB 8; Length 73921;
Best Local Similarity 94.4%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCGAACGTTCGAGATGAT 21
||||||| ||||||||||
Db 38151 TCGAACGGTCGAGATGAT 38134

RESULT 39
AK100785/c
LOCUS AK100785 1687 bp mRNA linear PLN 24-JUL-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J023120N10, full insert sequence.
ACCESSION AK100785
VERSION AK100785.1 GI:32985994
KEYWORDS FLI_CDNA; CAP trapper.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1
AUTHORS The Rice Full-Length cDNA Consortium, National Institute of

Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:, Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.

TITLE Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

JOURNAL Science 301 (5631), 376-379 (2003)

MEDLINE 22752273

PUBMED 12869764

REFERENCE 2 (bases 1 to 1687)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.

TITLE Direct Submission

JOURNAL Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

COMMENT This clone is one of the 28K full-length cDNA clones from japonica rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

FEATURES Location/Qualifiers
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/mol_type="mRNA"
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/clone="J023120N10"

ORIGIN

Query Match 77.1%; Score 16.2; DB 8; Length 1687;
Best Local Similarity 85.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 40
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LOCUS AF069993 2064 bp mRNA linear VRT 06-AUG-1999
DEFINITION Gallus gallus LIM domain interacting RING finger protein (R-LIM) mRNA, complete cds.
ACCESSION AF069993
VERSION AF069993.1 GI:4959045
KEYWORDS .
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 2064)

AUTHORS Bach,I., Rodriguez-Esteban,C., Carriere,C., Bhushan,A., Krones,A., Rose,D.W., Glass,C.K., Andersen,B., Izpisua Belmonte,J.C. and Rosenfeld,M.G.

TITLE RLIM inhibits functional activity of LIM homeodomain transcription factors via recruitment of the histone deacetylase complex

JOURNAL Nat. Genet. 22 (4), 394-399 (1999)

MEDLINE 99364422

PUBMED 10431247

REFERENCE 2 (bases 1 to 2064)

AUTHORS Bach,I.

TITLE Opposing Developmental Functions of Positive and Negative Coregulators of LIM Homeodomain Factors

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 2064)

AUTHORS Bach,I.

TITLE Direct Submission

JOURNAL Submitted (03-JUN-1998) Medicine, University of California at San Diego, 9500 Gilman Drive, La Jolla, CA 92093, USA

FEATURES Location/Qualifiers
source 1. .2064
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/mol_type="mRNA"
/db_xref="taxon:9031"
gene 1. .2064
/gene="R-LIM"
CDS 140. .1921
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/protein_id="AAD34210.1"
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EPSGGEDLENSQSDSEIPRSESPSVRQPGSERSTSEELTEEASPRGQRRARSRSPEQR
RTRARTDRSRSPINPVSEAPRRSHHNTSSQTFDHSAVNEAEGSSRTRQHVTLRQHAVG
TEIPSENAVLFSALETGPVPQAAGSSETNGASESAAPGQRPPTIVLDLQVRRVRPGEY

RQRDSIANRTRSRSQTPNNTVTYESERGGFRRTFSRSERAGVRTYVSTIRIPIRRILN
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SSNESTDVSSGEVFEGSNEGGSTSGARREGRNTRGSVTFEESGSLPFLSLAQFFLLNE
DDDDQPRGLTKEQIDNLAMRNFGETDALKTCSVCITEYTEGNKLRKLPCSHEYHVHCI
ARWLSENSTCPICRRAVLASGNRESVV"

ORIGIN

Query Match 77.1%; Score 16.2; DB 5; Length 2064;
Best Local Similarity 85.7%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Job time : 2885 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 5, 2004, 21:30:52 ; Search time 396 Seconds
(without alignments)
225.283 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgtcgaacgttcgagatgat 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	19	90.5	19	6	ABQ75170	Abq75170 ISS immun
	3	19	90.5	19	7	ACC49937	Acc49937 Human imm
	4	19	90.5	19	8	ADB88838	Adb88838 Chimeric
	5	19	90.5	22	6	ABQ75181	Abq75181 ISS immun
	6	19	90.5	22	8	ADB88849	Adb88849 Chimeric
	7	18	85.7	19	6	ABQ75175	Abq75175 ISS immun
	8	18	85.7	19	8	ADB88843	Adb88843 Chimeric
	9	17.4	82.9	19	6	ABQ75221	Abq75221 ISS immun
	10	17.4	82.9	19	6	ABQ75222	Abq75222 ISS immun
	11	17.4	82.9	19	8	ADB88891	Adb88891 Chimeric
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	13	17	81.0	19	6	ABQ75174	Abq75174 ISS immun
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c	18	16.4	78.1	23	3	AAA38067	Aaa38067 Immunosti
c	19	16.4	78.1	23	4	AAH75994	Aah75994 Immunomod
c	20	16.4	78.1	23	4	AAF77042	Aaf77042 Immunosti
c	21	16.4	78.1	23	5	AAH41575	Aah41575 Immunosti
c	22	16.4	78.1	23	5	AAS14666	Aas14666 Immunosti
c	23	16.4	78.1	23	6	ABA03835	Aba03835 Immunosti
c	24	16.4	78.1	23	6	ABA03846	Aba03846 Immunosti
c	25	16.4	78.1	23	6	AAS16339	Aas16339 ISS polyn
c	26	16.4	78.1	23	6	AAS16350	Aas16350 ISS polyn
c	27	16.4	78.1	23	6	ABA03858	Aba03858 Immunosti
c	28	16.2	77.1	1017	4	ABL12595	Abl12595 Drosophil
	29	16.2	77.1	1020	7	ACA47671	Aca47671 Prokaryot
c	30	16.2	77.1	1676	6	ABQ14749	Abq14749 Oligonucl
	31	16.2	77.1	1676	6	ABQ14748	Abq14748 Oligonucl
	32	16.2	77.1	3017	4	ABL12594	Abl12594 Drosophil
c	33	16.2	77.1	3126	7	ACA33960	Aca33960 Prokaryot
c	34	16.2	77.1	3135	9	ADC91948	Adc91948 E. faeciu
c	35	16.2	77.1	4024	2	AAV17086	Aav17086 Bos tauru
	36	16	76.2	66	8	ADB88936	Adb88936 Chimeric
	37	15.8	75.2	19	6	ABQ75223	Abq75223 ISS immun
	38	15.8	75.2	19	8	ADB88893	Adb88893 Chimeric
c	39	15.8	75.2	2726	4	ABL09441	Abl09441 Drosophil
c	40	15.8	75.2	5080	4	ABL09440	Abl09440 Drosophil
	41	15.8	75.2	6128	6	ABQ67039	Abq67039 Human ang
	42	15.8	75.2	6129	6	ABK31236	Abk31236 Signal tr
	43	15.8	75.2	6129	6	ABL70537	Abl70537 Chemicall
	44	15.8	75.2	6129	6	AAS61149	Aas61149 Human gen
c	45	15.8	75.2	11131	4	ABL09428	Abl09428 Drosophil

ALIGNMENTS

RESULT 1
ABQ75182
ID ABQ75182 standard; DNA; 21 BP.
XX
AC ABQ75182;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:132.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Claim 4; Page 21; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,

CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from the
CC present invention
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
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Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 2
ABQ75170
ID ABQ75170 standard; DNA; 19 BP.
XX
AC ABQ75170;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:19.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Claim 4; Page 20; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from the
CC present invention
XX
SQ Sequence 19 BP; 4 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 90.5%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
|||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATG 19

RESULT 3
ACC49937
ID ACC49937 standard; DNA; 19 BP.
XX
AC ACC49937;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human immunomodulatory polynucleotide SEQ ID NO: 11.
XX
KW Human; IMP; immunomodulatory polynucleotide; microcarrier complex;
KW antiasthmatic; antiallergic; antiinflammatory; cytostatic; virucide;
KW hepatotropic; protozoacide; antiulcer; dermatological; immune response;
KW interferon-gamma; interferon-alpha; IgEF; vaccine; asthma; rhinitis;
KW allergic conjunctivitis; cancer; infectious disease; viral infection;
KW parasitic infection; inflammatory disorder; ss.
XX
OS Homo sapiens.
XX
PN WO2003015816-A1.
XX
PD 27-FEB-2003.
XX
PF 13-AUG-2001; 2001WO-US025364.
XX
PR 10-AUG-2001; 2001US-00927422.
PR 10-AUG-2001; 2001US-00927884.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Van Nest G, Tuck S, Fearon KL, Dina D;
XX
DR WPI; 2003-312719/30.
XX
PT Immunomodulatory polynucleotide/microcarrier complexes that can increase
PT levels of interferon-gamma and interferon-alpha and reduce levels of
PT IgEF, comprises heptameric oligonucleotides.
XX
PS Example 5; Page 61; 84pp; English.
XX
CC The invention relates to novel immunomodulatory polynucleotide/
CC microcarrier complexes comprising heptameric oligonucleotides comprising
CC a 5' CG-3' sequence. A complex of the invention has antiasthmatic,
CC antiallergic, antiinflammatory, cytostatic, virucide, hepatotropic,
CC protozoacide, antiulcer, and dermatological activity. The complexes are
CC useful for modulating an immune response, increasing interferon-gamma,
CC increasing interferon-alpha, and reducing levels of IgEF. The complexes
CC can also be used in vaccines, to treat, for example, asthma, rhinitis,

CC allergic conjunctivitis, cancer, infectious diseases, viral infections,
CC parasitic infections (e.g. malaria, leishmaniasis), inflammatory
CC disorders (e.g. ulcerative colitis, idiopathic pulmonary fibrosis,
CC scleroderma). The present sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 19 BP; 4 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 90.5%; Score 19; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATG 19

RESULT 4
ADB88838
ID ADB88838 standard; DNA; 19 BP.
XX
AC ADB88838;
XX
DT 04-DEC-2003 (first entry)
XX
DE Chimeric immunomodulatory compound DNA sequence, SEQ ID No 41.
XX
KW chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW immunoglobulin E; IgE; allergy; cancer;
KW stimulating cellular immune system cell; ss.
XX
OS Synthetic.
XX
PN WO2003000922-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US020025.
XX
PR 21-JUN-2001; 2001US-0299883P.
PR 23-APR-2002; 2002US-0375253P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D, Tuck SF;
XX
DR WPI; 2003-210159/20.
XX
PT Novel chimeric immunomodulatory compound having immunomodulatory
PT activity, useful for modulating an immune response and for treating
PT cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS Disclosure; Page 33; 224pp; English.
XX
CC The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC having immunomodulatory activity, comprising two or more nucleic acid
CC moieties and one or more non-nucleic acid spacer moieties, where at least
CC one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC acid moieties, where the spacer is not a polypeptide, and at least one
CC nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC immunodulatory compounds more specifically contain the nucleic acid
CC spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC CIC's are useful for modulating an immune response in an individual,
CC where the individual suffers from a disorder associated with a Th2-type
CC immune response which is an allergy or allergy-induced asthma, and an
CC infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC alpha; in an individual, where the individual has idiopathic pulmonary
CC fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC disorder in an individual, where the IgE-related disorder is allergy, or
CC an allergy-related disorder. CIC's are also useful for treating cancer
CC and can be used for stimulating cellular immune system cells production
CC in an individual. This polynucleotide sequence represents a DNA sequence
CC which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC of the invention.
XX
SQ Sequence 19 BP; 4 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 90.5%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATG 19

RESULT 5
ABQ75181
ID ABQ75181 standard; DNA; 22 BP.
XX
AC ABQ75181;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:30.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Disclosure; Page 21; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a

CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from the
CC present invention
XX
SQ Sequence 22 BP; 5 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 90.5%; Score 19; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||||||||||||||||
Db 4 TCGTCGAACGTTCGAGATG 22

RESULT 6
ADB88849
ID ADB88849 standard; DNA; 22 BP.
XX
AC ADB88849;
XX
DT 04-DEC-2003 (first entry)
XX
DE Chimeric immunomodulatory compound DNA sequence, SEQ ID No 52.
XX
KW chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW immunoglobulin E; IgE; allergy; cancer;
KW stimulating cellular immune system cell; ss.
XX
OS Synthetic.
XX
PN WO2003000922-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US020025.
XX
PR 21-JUN-2001; 2001US-0299883P.
PR 23-APR-2002; 2002US-0375253P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D, Tuck SF;
XX
DR WPI; 2003-210159/20.
XX
PT Novel chimeric immunomodulatory compound having immunomodulatory
PT activity, useful for modulating an immune response and for treating
PT cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS Disclosure; Page 34; 224pp; English.
XX
CC The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC having immunomodulatory activity, comprising two or more nucleic acid
CC moieties and one or more non-nucleic acid spacer moieties, where at least
CC one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC acid moieties, where the spacer is not a polypeptide, and at least one
CC nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC immunodulatory compounds more specifically contain the nucleic acid
CC spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC CIC's are useful for modulating an immune response in an individual,
CC where the individual suffers from a disorder associated with a Th2-type
CC immune response which is an allergy or allergy-induced asthma, and an
CC infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC alpha; in an individual, where the individual has idiopathic pulmonary
CC fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC disorder in an individual, where the IgE-related disorder is allergy, or
CC an allergy-related disorder. CIC's are also useful for treating cancer
CC and can be used for stimulating cellular immune system cells production
CC in an individual. This polynucleotide sequence represents a DNA sequence
CC which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC of the invention.
XX
SQ Sequence 22 BP; 5 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 90.5%; Score 19; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||||||||||||||||
Db 4 TCGTCGAACGTTCGAGATG 22

RESULT 7
ABQ75175
ID ABQ75175 standard; DNA; 19 BP.
XX
AC ABQ75175;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:24.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-bromocytosine"
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Example 1; Page 20; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an

CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from the
CC present invention
XX
SQ Sequence 19 BP; 4 A; 3 C; 6 G; 5 T; 0 U; 1 Other;

Query Match 85.7%; Score 18; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||||||||||||||
Db 1 TCGTNGAACGTTCGAGATG 19

RESULT 8
ADB88843
ID ADB88843 standard; DNA; 19 BP.
XX
AC ADB88843;
XX
DT 04-DEC-2003 (first entry)
XX
DE Chimeric immunomodulatory compound DNA sequence, SEQ ID No 46.
XX
KW chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW immunoglobulin E; IgE; allergy; cancer;
KW stimulating cellular immune system cell; ss.
XX
OS Synthetic.
XX
PN WO2003000922-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US020025.
XX
PR 21-JUN-2001; 2001US-0299883P.
PR 23-APR-2002; 2002US-0375253P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D, Tuck SF;
XX
DR WPI; 2003-210159/20.
XX
PT Novel chimeric immunomodulatory compound having immunomodulatory
PT activity, useful for modulating an immune response and for treating
PT cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS Disclosure; Page 33; 224pp; English.
XX
CC The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC having immunomodulatory activity, comprising two or more nucleic acid
CC moieties and one or more non-nucleic acid spacer moieties, where at least
CC one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC acid moieties, where the spacer is not a polypeptide, and at least one
CC nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC immunodulatory compounds more specifically contain the nucleic acid
CC spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC CIC's are useful for modulating an immune response in an individual,
CC where the individual suffers from a disorder associated with a Th2-type
CC immune response which is an allergy or allergy-induced asthma, and an
CC infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC alpha; in an individual, where the individual has idiopathic pulmonary
CC fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC disorder in an individual, where the IgE-related disorder is allergy, or
CC an allergy-related disorder. CIC's are also useful for treating cancer
CC and can be used for stimulating cellular immune system cells production
CC in an individual. This polynucleotide sequence represents a DNA sequence
CC which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC of the invention.
XX
SQ Sequence 19 BP; 4 A; 3 C; 6 G; 5 T; 0 U; 1 Other;

Query Match 85.7%; Score 18; DB 8; Length 19;
Best Local Similarity 94.7%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||||||||||||||
Db 1 TCGTNGAACGTTCGAGATG 19

RESULT 9
ABQ75221
ID ABQ75221 standard; DNA; 19 BP.
XX
AC ABQ75221;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:56.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Disclosure; Page 22; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an

CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from the
CC present invention
XX
SQ Sequence 19 BP; 3 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 82.9%; Score 17.4; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||| ||||||||||||
Db 1 TCGTCGGACGTTCGAGATG 19

RESULT 10
ABQ75222
ID ABQ75222 standard; DNA; 19 BP.
XX
AC ABQ75222;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:57.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Disclosure; Page 22; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from the
CC present invention
XX
SQ Sequence 19 BP; 3 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 82.9%; Score 17.4; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||| ||||||||||||
Db 1 TCGTCGTACGTTCGAGATG 19

RESULT 11
ADB88891
ID ADB88891 standard; DNA; 19 BP.
XX
AC ADB88891;
XX
DT 04-DEC-2003 (first entry)
XX
DE Chimeric immunomodulatory compound DNA sequence, SEQ ID No 94.
XX
KW chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW immunoglobulin E; IgE; allergy; cancer;
KW stimulating cellular immune system cell; ss.
XX
OS Synthetic.
XX
PN WO2003000922-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US020025.
XX
PR 21-JUN-2001; 2001US-0299883P.
PR 23-APR-2002; 2002US-0375253P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D, Tuck SF;
XX
DR WPI; 2003-210159/20.
XX
PT Novel chimeric immunomodulatory compound having immunomodulatory
PT activity, useful for modulating an immune response and for treating
PT cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS Disclosure; Page 35; 224pp; English.
XX
CC The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC having immunomodulatory activity, comprising two or more nucleic acid
CC moieties and one or more non-nucleic acid spacer moieties, where at least
CC one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC acid moieties, where the spacer is not a polypeptide, and at least one
CC nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC immunodulatory compounds more specifically contain the nucleic acid
CC spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC CIC's are useful for modulating an immune response in an individual,
CC where the individual suffers from a disorder associated with a Th2-type
CC immune response which is an allergy or allergy-induced asthma, and an
CC infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC alpha; in an individual, where the individual has idiopathic pulmonary
CC fibrosis, or a viral infection. CIC's are useful for ameliorating a

```
CC   symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC   disorder in an individual, where the IgE-related disorder is allergy, or
CC   an allergy-related disorder. CIC's are also useful for treating cancer
CC   and can be used for stimulating cellular immune system cells production
CC   in an individual. This polynucleotide sequence represents a DNA sequence
CC   which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC   of the invention.
XX
SQ   Sequence 19 BP; 3 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             82.9%;  Score 17.4;  DB 8;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 21;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||| ||||||||||||
Db          1 TCGTCGGACGTTCGAGATG 19


RESULT 12
ADB88892
ID   ADB88892 standard; DNA; 19 BP.
XX
AC   ADB88892;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Chimeric immunomodulatory compound DNA sequence, SEQ ID No 95.
XX
KW   chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW   spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW   Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW   IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW   immunoglobulin E; IgE; allergy; cancer;
KW   stimulating cellular immune system cell; ss.
XX
OS   Synthetic.
XX
PN   WO2003000922-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US020025.
XX
PR   21-JUN-2001; 2001US-0299883P.
PR   23-APR-2002; 2002US-0375253P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D,  Tuck SF;
XX
DR   WPI; 2003-210159/20.
XX
PT   Novel chimeric immunomodulatory compound having immunomodulatory
PT   activity, useful for modulating an immune response and for treating
PT   cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS   Disclosure; Page 35; 224pp; English.
XX
CC   The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC   having immunomodulatory activity, comprising two or more nucleic acid
CC   moieties and one or more non-nucleic acid spacer moieties, where at least
CC   one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC   acid moieties, where the spacer is not a polypeptide, and at least one
CC   nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC   immunodulatory compounds more specifically contain the nucleic acid
CC   spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC   CIC's are useful for modulating an immune response in an individual,
CC   where the individual suffers from a disorder associated with a Th2-type
CC   immune response which is an allergy or allergy-induced asthma, and an
CC   infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC   alpha; in an individual, where the individual has idiopathic pulmonary
CC   fibrosis, or a viral infection. CIC's are useful for ameliorating a
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CC   symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC   disorder in an individual, where the IgE-related disorder is allergy, or
CC   an allergy-related disorder. CIC's are also useful for treating cancer
CC   and can be used for stimulating cellular immune system cells production
CC   in an individual. This polynucleotide sequence represents a DNA sequence
CC   which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC   of the invention.
XX
SQ   Sequence 19 BP; 3 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match             82.9%;  Score 17.4;  DB 8;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 21;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||| ||||||||||||
Db          1 TCGTCGTACGTTCGAGATG 19


RESULT 13
ABQ75174
ID   ABQ75174 standard; DNA; 19 BP.
XX
AC   ABQ75174;
XX
DT   05-NOV-2002  (first entry)
XX
DE   ISS immunomodulatory oligonucleotide SEQ ID NO:23.
XX
KW   Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW   allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW   idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW   malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW   immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW   virucide; antibacterial; protozoacide; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   2
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-bromocytosine"
FT   modified_base   5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "5-bromocytosine"
XX
PN   WO200252002-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-US050821.
XX
PR   27-DEC-2000; 2000US-0258675P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D;
XX
DR   WPI; 2002-657426/70.
XX
PT   Immunomodulatory polynucleotide for modulating an immune response in a
PT   subject suffering from disorders associated with Th2-type immune
PT   response, e.g. allergy, or infectious disease, comprises an
PT   immunostimulatory sequence.
XX
PS   Example 1; Page 20; 95pp; English.
XX
CC   The present invention describes an immunomodulatory polynucleotide (I)
CC   comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC   immunomodulatory composition comprising (I); (2) an immunomodulatory
CC   polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
```

CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from the
CC present invention
XX
SQ Sequence 19 BP; 4 A; 2 C; 6 G; 5 T; 0 U; 2 Other;

Query Match 81.0%; Score 17; DB 6; Length 19;
Best Local Similarity 89.5%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
| || ||||||||||||||
Db 1 TNGTNGAACGTTCGAGATG 19

RESULT 14
ADB88842
ID ADB88842 standard; DNA; 19 BP.
XX
AC ADB88842;
XX
DT 04-DEC-2003 (first entry)
XX
DE Chimeric immunomodulatory compound DNA sequence, SEQ ID No 45.
XX
KW chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW immunoglobulin E; IgE; allergy; cancer;
KW stimulating cellular immune system cell; ss.
XX
OS Synthetic.
XX
PN WO2003000922-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US020025.
XX
PR 21-JUN-2001; 2001US-0299883P.
PR 23-APR-2002; 2002US-0375253P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D, Tuck SF;
XX
DR WPI; 2003-210159/20.
XX
PT Novel chimeric immunomodulatory compound having immunomodulatory
PT activity, useful for modulating an immune response and for treating
PT cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS Disclosure; Page 33; 224pp; English.
XX
CC The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC having immunomodulatory activity, comprising two or more nucleic acid
CC moieties and one or more non-nucleic acid spacer moieties, where at least
CC one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC acid moieties, where the spacer is not a polypeptide, and at least one
CC nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC immunodulatory compounds more specifically contain the nucleic acid
CC spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC CIC's are useful for modulating an immune response in an individual,
CC where the individual suffers from a disorder associated with a Th2-type
CC immune response which is an allergy or allergy-induced asthma, and an
CC infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC alpha; in an individual, where the individual has idiopathic pulmonary
CC fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC disorder in an individual, where the IgE-related disorder is allergy, or
CC an allergy-related disorder. CIC's are also useful for treating cancer
CC and can be used for stimulating cellular immune system cells production
CC in an individual. This polynucleotide sequence represents a DNA sequence
CC which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC of the invention.
XX
SQ Sequence 19 BP; 4 A; 2 C; 6 G; 5 T; 0 U; 2 Other;

Query Match 81.0%; Score 17; DB 8; Length 19;
Best Local Similarity 89.5%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
| || ||||||||||||||
Db 1 TNGTNGAACGTTCGAGATG 19

RESULT 15
ABQ75165
ID ABQ75165 standard; DNA; 18 BP.
XX
AC ABQ75165;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:14.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US050821.
XX
PR 27-DEC-2000; 2000US-0258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Example 1; Page 20; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and

CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from the
CC present invention
XX
SQ Sequence 18 BP; 4 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 78.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGTCGAACGTTCGAGATG 19
| ||||||||||||||||
Db 1 CTTCGAACGTTCGAGATG 18

RESULT 16
ADB88833
ID ADB88833 standard; DNA; 18 BP.
XX
AC ADB88833;
XX
DT 04-DEC-2003 (first entry)
XX
DE Chimeric immunomodulatory compound DNA sequence, SEQ ID No 36.
XX
KW chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW immunoglobulin E; IgE; allergy; cancer;
KW stimulating cellular immune system cell; ss.
XX
OS Synthetic.
XX
PN WO2003000922-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US020025.
XX
PR 21-JUN-2001; 2001US-0299883P.
PR 23-APR-2002; 2002US-0375253P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D, Tuck SF;
XX
DR WPI; 2003-210159/20.
XX
PT Novel chimeric immunomodulatory compound having immunomodulatory
PT activity, useful for modulating an immune response and for treating
PT cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS Disclosure; Page 33; 224pp; English.
XX
CC The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC having immunomodulatory activity, comprising two or more nucleic acid
CC moieties and one or more non-nucleic acid spacer moieties, where at least
CC one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC acid moieties, where the spacer is not a polypeptide, and at least one
CC nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC immunomodulatory compounds more specifically contain the nucleic acid
CC spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC CIC's are useful for modulating an immune response in an individual,
CC where the individual suffers from a disorder associated with a Th2-type
CC immune response which is an allergy or allergy-induced asthma, and an
CC infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC alpha; in an individual, where the individual has idiopathic pulmonary
CC fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC disorder in an individual, where the IgE-related disorder is allergy, or
CC an allergy-related disorder. CIC's are also useful for treating cancer
CC and can be used for stimulating cellular immune system cells production
CC in an individual. This polynucleotide sequence represents a DNA sequence
CC which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC of the invention.
XX
SQ Sequence 18 BP; 4 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 78.1%; Score 16.4; DB 8; Length 18;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGTCGAACGTTCGAGATG 19
| ||||||||||||||||
Db 1 CTTCGAACGTTCGAGATG 18

RESULT 17
AAV80098/c
ID AAV80098 standard; DNA; 23 BP.
XX
AC AAV80098;
XX
DT 12-MAR-1999 (first entry)
XX
DE Immunomodulatory oligo comprising an ISS sequence.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS Synthetic.
XX
PN WO9855495-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US011578.
XX
PR 06-JUN-1997; 97US-0048793P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Schwartz D, Roman M, Dina D;
XX
DR WPI; 1999-059898/05.
XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases.
XX
PS Claim 6; Page 29; 63pp; English.
XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and

```
CC   Schistosoma. The immunomodulatory sequences are used to screen for human
CC   immunostimulatory activity by incubating macrophage cells and the
CC   oligonucleotide; and determining the relative amount of Th1-biased
CC   cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC   specific claimed examples of such immunomodulatory oligonucleotides
XX
SQ   Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             78.1%;  Score 16.4;  DB 2;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 72;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 18
AAA38067/c
ID   AAA38067 standard; DNA; 23 BP.
XX
AC   AAA38067;
XX
DT   24-AUG-2000  (first entry)
XX
DE   Immunostimulatory sequence (ISS) #3.
XX
KW   Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
KW   gp120; human immunodeficiency virus; HIV; immune response; infection;
KW   development; ss.
XX
OS   Synthetic.
XX
PN   WO200021556-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US023677.
XX
PR   09-OCT-1998;   98US-0103733P.
PR   07-OCT-1999;   99US-00415186.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Tighe H,  Raz E,  Schwartz D,  Takabayashi K;
XX
DR   WPI; 2000-317846/27.
XX
PT   Anti-HIV composition comprises immunostimulatory polynucleotides and HIV
PT   glycoprotein gp120 useful for modulating, stimulating an immune response
PT   against HIV in an HIV infected individual.
XX
PS   Disclosure; Page 16; 65pp; English.
XX
CC   The present invention relates to an immunostimulatory composition
CC   comprising a human immunodeficiency virus (HIV) antigen, and an
CC   immunomodulatory polynucleotide comprising an immunostimulatory sequence
CC   (ISS). This sequence represents an ISS that can be used in the
CC   composition. An immunostimulatory composition which comprises a gp120
CC   conjugated to an immunomodulatory polynucleotide, or is proximately
CC   associated to it and not conjugated, is used for modulating or
CC   stimulating a specific immune response against gp120 in an individual by
CC   producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC   is also used for suppressing or delaying development of HIV infection in
CC   an individual infected with HIV or an individual at risk of infection
CC   with HIV, respectively. It is also used for treating an individual
CC   infected with HIV in need of immune modulation
XX
SQ   Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             78.1%;  Score 16.4;  DB 3;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 72;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 19
AAH75994/c
ID   AAH75994 standard; DNA; 23 BP.
XX
AC   AAH75994;
XX
DT   15-NOV-2001  (first entry)
XX
DE   Immunomodulatory oligonucleotide #3.
XX
KW   Immunomodulatory; immunostimulatory; Th1-type immune response;
KW   Th2-type immune response; interferon; idiopathic pulmonary fibrosis;
KW   viral infection; ss.
XX
OS   Synthetic.
XX
PN   WO200168143-A2.
XX
PD   20-SEP-2001.
XX
PF   12-MAR-2001; 2001WO-US007843.
XX
PR   10-MAR-2000; 2000US-0188557P.
PR   09-MAR-2001; 2001US-00802376.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Van Nest G,  Tuck S;
XX
DR   WPI; 2001-582389/65.
XX
PT   Immunomodulatory polynucleotide/microcarrier complexes comprise an
PT   immunostimulatory sequence containing polynucleotide linked to a
PT   nonbiodegradable microcarrier.
XX
PS   Disclosure; Page 18; 61pp; English.
XX
CC   The present invention relates to immunomodulatory polynucleotide/
CC   microcarrier complexes. The complexes comprise an immunostimulatory
CC   sequence (ISS), e.g. the present sequence, linked to a nonbiodegradable
CC   microcarrier provided that if the microcarrier is gold, latex or magnetic
CC   then the linkage is not biotin/avidin. The complex is useful for
CC   modulating an immune response (especially stimulating a Th1-type response
CC   or suppressing a Th2-type response), increasing interferon-gamma
CC   (especially in a patient suffering from idiopathic pulmonary fibrosis),
CC   increasing interferon-alpha (especially in patients suffering from viral
CC   infection) and reducing levels of IgE
XX
SQ   Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             78.1%;  Score 16.4;  DB 4;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 72;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 20
AAF77042/c
ID   AAF77042 standard; DNA; 23 BP.
XX
AC   AAF77042;
XX
DT   15-MAY-2001  (first entry)
XX
```

DE Immunostimulatory DNA #2.
XX
KW Modulate; immune; antigen; immunostimulatory; ds.
XX
OS Synthetic.
XX
PN WO200112223-A2.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000WO-US022835.
XX
PR 19-AUG-1999; 99US-0149768P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Van Nest G;
XX
DR WPI; 2001-211136/21.
XX
PT Modulating immune response to a second antigen in humans involves
PT administering an immunostimulatory polynucleotide comprising an
PT immunostimulatory sequence and a first antigen.
XX
PS Disclosure; Page 15; 63pp; English.
XX
CC The present invention relates to modulating an immune response to a
CC second antigen in an individual, involving administering to the
CC individual an immunomodulatory polynucleotide comprising an
CC immunostimulatory sequence (ISS) and a first antigen
XX
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 78.1%; Score 16.4; DB 4; Length 23;
Best Local Similarity 94.4%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCGAACGTTCGAGATGA 20
|| ||||||||||||||||
Db 18 GTGGAACGTTCGAGATGA 1

RESULT 21
AAH41575/c
ID AAH41575 standard; DNA; 23 BP.
XX
AC AAH41575;
XX
DT 24-AUG-2001 (first entry)
XX
DE Immunostimulatory sequence (ISS) SEQ ID NO:3.
XX
KW Immunostimulatory sequence; ISS; immunomodulatory; immune response;
KW antigen; antiallergic; modulation; Th1 lymphocyte stimulation; allergy;
KW Th1-associated cytokine; Th2 lymphocyte suppression; cytokine; ss.
XX
OS Synthetic.
XX
PN WO200135991-A2.
XX
PD 25-MAY-2001.
XX
PF 15-NOV-2000; 2000WO-US031385.
XX
PR 15-NOV-1999; 99US-0165467P.
PR 14-NOV-2000; 2000US-00713136.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Tuck S, Van Nest G;
XX
DR WPI; 2001-329209/34.
XX
PT Populations of conjugate molecules comprising polynucleotide
PT immunostimulatory sequences polynucleotides and antigens, useful for
PT controlling immune responses.
XX
PS Disclosure; Page 30; 97pp; English.
XX
CC The present invention describes immunomodulatory populations ((I) and
CC (II)) of conjugate molecules (CMs) comprising immunostimulatory sequences
CC (ISS) of polynucleotides and antigens. The extent of conjugation affects
CC the immunological properties (e.g. the extent of antigen-specific
CC antibody formation, including Th1-associated antibody formation) so the
CC conjugates are used for altering the type and extent of immune response.
CC (I) and (II) have immunomodulatory, immunosuppressive and antiallergic
CC activities, and can be used in the modulation of immune responses via the
CC stimulation of Th1 lymphocytes and Th1-associated cytokines, and
CC suppression of Th2 lymphocytes and cytokines. The populations ((I) and
CC (II)) of conjugate molecules may be used for modulating immune responses
CC in individuals e.g. for the treatment of an allergic condition. (I) and
CC (II) may be used to modulate immune responses and therefore prevent
CC potentially harmful reactions to antigens. The present sequence
CC represents an ISS polynucleotide which is used in the exemplification of
CC the present invention
XX
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 78.1%; Score 16.4; DB 5; Length 23;
Best Local Similarity 94.4%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCGAACGTTCGAGATGA 20
|| ||||||||||||||||
Db 18 GTGGAACGTTCGAGATGA 1

RESULT 22
AAS14666/c
ID AAS14666 standard; DNA; 23 BP.
XX
AC AAS14666;
XX
DT 18-DEC-2001 (first entry)
XX
DE Immunostimulatory sequence, ISS #3.
XX
KW Immunostimulatory sequence; ISS; ds; antiviral; immunogen;
KW respiratory syncytial virus; RSV; influenza virus; rhinovirus;
KW adenovirus; measles virus; mumps virus; parainfluenza virus;
KW rubella virus; poxvirus; parvovirus; hantavirus; varicella virus.
XX
OS Respiratory syncytial virus.
OS Synthetic.
XX
PN WO200168116-A2.
XX
PD 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-US007839.
XX
PR 10-MAR-2000; 2000US-0188583P.
PR 09-MAR-2001; 2001US-00802686.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Van Nest G;
XX
DR WPI; 2001-607438/69.
XX
PT Suppressing a respiratory syncytial virus infection by administering an
PT immunostimulatory sequence at the site of infection is useful to prevent
PT and treat lower respiratory tract viral infections.
XX
PS Disclosure; Page 15; 40pp; English.
XX

CC The invention relates to suppressing a respiratory syncytial virus (RSV)
CC infection in an exposed individual, comprising administering a
CC polynucleotide comprising an immunostimulatory sequence (ISS) comprising
CC the sequence 5'-C, G-3', where an RSV antigen is not administered. The
CC invention is used to prevent and treat respiratory syncytial virus
CC infection of the lower respiratory tract and other viruses including
CC influenza virus, rhinovirus, adenovirus, measles virus, mumps virus,
CC parainfluenza virus, rubella virus, poxvirus, parvovirus, hantavirus and
CC varicella virus. A kit for carrying out the administration is also
CC included. Unlike the prior art antiviral agent ribavirin, which is a
CC potential teratogen, the invention provides a treatment which does not
CC carry unacceptable side effects. Other prior art medicaments treat the
CC symptoms only, whilst the invention treats the infection. The present
CC sequence is an ISS of the invention
XX
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 78.1%; Score 16.4; DB 5; Length 23;
Best Local Similarity 94.4%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCGAACGTTCGAGATGA 20
|| ||||||||||||||||
Db 18 GTGGAACGTTCGAGATGA 1

RESULT 23
ABA03835/c
ID ABA03835 standard; DNA; 23 BP.
XX
AC ABA03835;
XX
DT 12-FEB-2002 (first entry)
XX
DE Immunostimulatory sequence (ISS) SEQ ID NO:3.
XX
KW Immunomodulatory polynucleotide/microcarrier complex; IMP/MC; IgE;
KW immunomodulation; immunostimulation; phosphorothioate; immunomodulator;
KW antiallergic; antibacterial; antiprotozoal; antiparasitic; hepatotropic;
KW nephrotropic; interferon-alpha stimulator; interferon-gamma stimulator;
KW immunoglobulin E stimulator; immune response; IPF; scleroderma; malaria;
KW idiopathic pulmonary fibrosis; cutaneous radiation-induced fibrosis;
KW hepatic fibrosis; renal fibrosis; infectious disease; leishmaniasis;
KW mycobacterial disease; toxoplasmosis; schistosomiasis; chlonorchiasis;
KW allergy; allergy-induced asthma; prophylactic vaccine; cancer; ss.
XX
OS Synthetic.
XX
PN WO200168144-A2.
XX
PD 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-US007848.
XX
PR 10-MAR-2000; 2000US-0188303P.
PR 09-MAR-2001; 2001US-00802359.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Van Nest G, Tuck S;
XX
DR WPI; 2002-049002/06.
XX
PT New immunomodulatory polynucleotide/microcarrier complex, useful for
PT modulating the immune response of individuals, particularly humans, or
PT for treating idiopathic pulmonary fibrosis, scleroderma, malaria or
PT allergies.
XX
PS Disclosure; Page 18; 63pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide/
CC microcarrier (IMP/MC) complex (I), which comprises a polynucleotide
CC having an immunostimulatory sequence (ISS) linked to a biodegradable
CC microcarrier (MC). The ISS comprises the sequence: 5'-CG-3', where the MC
CC is less than 10 micro m in size. (I) has immunomodulator, antiallergic,
CC antibacterial, antiprotozoal, antiparasitic, hepatotropic and
CC nephrotropic activities. It can be used as an interferon (IFN)-alpha
CC stimulator, IFN-gamma stimulator or an immunoglobulin E (IgE) stimulator.
CC (I) can be used for modulating the immune response of individuals,
CC particularly humans. The IMP/MC complex is particularly useful for
CC treating idiopathic pulmonary fibrosis (IPF), scleroderma, cutaneous
CC radiation-induced fibrosis, hepatic fibrosis including schistosomiasis-
CC induced hepatic fibrosis, renal fibrosis, infectious diseases caused by
CC cellular pathogen (e.g. a mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis or chlonorchiasis), or disorders
CC associated with a Th2-type immune response (e.g. allergies or allergy-
CC induced asthma). The IMP/MC may also be used in individuals receiving
CC therapeutic or prophylactic vaccines, in individuals suffering from
CC cancer, or in individuals at risk of exposure to an infectious agent. The
CC present sequence represents an ISS given in the exemplification of the
CC present invention
XX
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 78.1%; Score 16.4; DB 6; Length 23;
Best Local Similarity 94.4%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCGAACGTTCGAGATGA 20
|| ||||||||||||||||
Db 18 GTGGAACGTTCGAGATGA 1

RESULT 24
ABA03846/c
ID ABA03846 standard; DNA; 23 BP.
XX
AC ABA03846;
XX
DT 12-FEB-2002 (first entry)
XX
DE Immunostimulatory sequence (ISS) SEQ ID NO:3.
XX
KW Immunostimulatory sequence; ISS; immunostimulation; viral infection;
KW immunomodulation; virucide; gene therapy; viraemia; ss.
XX
OS Synthetic.
XX
PN WO200168077-A2.
XX
PD 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-US007840.
XX
PR 10-MAR-2000; 2000US-0188302P.
PR 09-MAR-2001; 2001US-00802685.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Van Nest G;
XX
DR WPI; 2002-048999/06.
XX
PT Reducing severity, recurrence or duration of symptom of virus infection,
PT or reducing viremia or blood levels of virus antigen, comprises
PT administering a polynucleotide having an immunostimulatory sequence.
XX
PS Disclosure; Page 20; 65pp; English.
XX
CC The present invention describes a method for reducing severity of a
CC symptom of virus infection in an individual infected with a virus. The
CC method comprises administering a composition consisting of a
CC polynucleotide having an immunostimulatory sequence (ISS). The ISS
CC comprises the sequence 5'-C,G,pyrimidine,pyrimidine,C,G-3'. An antigen is
CC administered in conjunction with the composition. ISS has virucide
CC activity and can be used in gene therapy. The method using the ISS can be

CC used for suppressing, ameliorating and/or preventing viral infections to
CC an individual who may be at risk of being exposed to, exposed to or
CC infected by a virus. It may also be used in reducing the recurrence or
CC duration of a symptom of viral infection, delaying the development of a
CC virus infection, and reducing viraemia or blood levels of virus antigens.
CC The present sequence represents an ISS given in the exemplification of
CC the present invention
XX
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 78.1%; Score 16.4; DB 6; Length 23;
Best Local Similarity 94.4%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCGAACGTTCGAGATGA 20
|| ||||||||||||||||
Db 18 GTGGAACGTTCGAGATGA 1

RESULT 25
AAS16339/c
ID AAS16339 standard; DNA; 23 BP.
XX
AC AAS16339;
XX
DT 14-FEB-2002 (first entry)
XX
DE ISS polynucleotide #3 useful for treating herpes virus infections.
XX
KW Herpes simplex virus; HSV infection; immunostimulatory sequence; ISS;
KW immune response; alphaherpesvirinae; herpes virus zoster virus; VZV;
KW HSV-1; HSV-2; chicken pox; herpes labialis; cold sore; genital herpes;
KW virucide; ss.
XX
OS Synthetic.
XX
PN WO200168103-A2.
XX
PD 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-US007841.
XX
PR 10-MAR-2000; 2000US-0188556P.
PR 09-MAR-2001; 2001US-00802518.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Van Nest G;
XX
DR WPI; 2002-041171/05.
XX
PT Preventing, reducing the severity or reducing the recurrence of an
PT infection or symptom of herpes simplex virus (HSV), e.g. HSV-2, comprises
PT administering an immunostimulatory sequence to an individual.
XX
PS Disclosure; Page 19; 49pp; English.
XX
CC The present invention relates to novel methods of treating, preventing,
CC or reducing the severity or recurrence of a symptom of herpes simplex
CC virus (HSV) infection in an individual who has been exposed to or who is
CC infected with HSV. The method comprises administering a polynucleotide
CC having an immunostimulatory sequence (ISS; AAS16337-AAS16345) which
CC induces an immune response. A composition containing ISS is administered
CC without a HSV (alphaherpesvirinae) antigen. The composition can be
CC included in a kit for ameliorating or preventing a symptom of HSV
CC infection caused by herpes virus zoster virus (VZV), HSV-1 and
CC particularly HSV-2. Such HSV infections include chicken pox, herpes
CC labialis (cold sores) and genital herpes. The present sequence represents
CC one of the ISS polynucleotides of the invention. Note: The present
CC sequence is shown as single stranded in the specification, but the
CC patentees state on page 20 that this sequence may be double stranded
XX
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 78.1%; Score 16.4; DB 6; Length 23;
Best Local Similarity 94.4%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCGAACGTTCGAGATGA 20
|| ||||||||||||||||
Db 18 GTGGAACGTTCGAGATGA 1

RESULT 26
AAS16350/c
ID AAS16350 standard; DNA; 23 BP.
XX
AC AAS16350;
XX
DT 14-FEB-2002 (first entry)
XX
DE ISS polynucleotide #3 useful for treating papillomavirus infections.
XX
KW Animal papillomavirus infection; human papillomavirus; HPV; STD; wart;
KW sexually transmitted disease; cervical cancer; immune response;
KW immunostimulatory sequence; ISS; virucide; ss.
XX
OS Synthetic.
XX
PN WO200168117-A2.
XX
PD 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-US007842.
XX
PR 10-MAR-2000; 2000US-0188265P.
PR 09-MAR-2001; 2001US-00802445.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Van Nest G;
XX
DR WPI; 2002-041172/05.
XX
PT Treating, preventing or ameliorating papillomavirus infections, comprises
PT administering a composition comprising a polynucleotide having an
PT immunostimulatory sequence to the individual.
XX
PS Disclosure; Page 20; 44pp; English.
XX
CC The present invention relates to novel methods of treating, preventing,
CC or reducing the severity or recurrence of a symptom of papillomavirus
CC infection in an individual that has been exposed to or who is infected
CC with papillomavirus. The method comprises administering a polynucleotide
CC having an immunostimulatory sequence (ISS; AAS16348-AAS16355) which
CC induces an immune response. A composition containing ISS is administered
CC without a papillomavirus antigen. The composition can be included in a
CC kit for ameliorating or preventing a symptom of human or animal
CC papillomavirus infection. Infections with human papillomavirus (HPV)
CC which can be prevented or treated using the method of the invention
CC include sexually transmitted diseases (STDs), warts, papillomas and
CC cervical cancer. The present sequence represents one of the ISS
CC polynucleotides of the invention. Note: The present sequence is shown as
CC single stranded in the specification, but the patentees state on page 20
CC that this sequence may be double stranded
XX
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 78.1%; Score 16.4; DB 6; Length 23;
Best Local Similarity 94.4%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCGAACGTTCGAGATGA 20
|| ||||||||||||||||
Db 18 GTGGAACGTTCGAGATGA 1

```
RESULT 27
ABA03858/c
ID   ABA03858 standard; DNA; 23 BP.
XX
AC   ABA03858;
XX
DT   12-FEB-2002  (first entry)
XX
DE   Immunostimulatory sequence (ISS) SEQ ID NO:3.
XX
KW   Immunostimulatory sequence; ISS; immunomodulation; HBV; HCV; infection;
KW   hepatitis B virus; hepatitis C virus; virucide; anti-inflammatory;
KW   hepatotropic; gene therapy; hepatitis infection; viraemia; jaundice;
KW   fatigue; abdominal pain; portal hypertension; cirrhosis; ss.
XX
OS   Synthetic.
XX
PN   WO200168078-A2.
XX
PD   20-SEP-2001.
XX
PF   12-MAR-2001; 2001WO-US007931.
XX
PR   10-MAR-2000; 2000US-0188301P.
PR   09-MAR-2001; 2001US-00802370.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Van Nest G;
XX
DR   WPI; 2002-049000/06.
XX
PT   Reducing viremia and blood levels of hepatitis virus antigen in an
PT   individual infected with hepatitis B virus, comprises administering a
PT   composition comprising a polynucleotide having an immunostimulatory
PT   sequence.
XX
PS   Disclosure; Page 20; 43pp; English.
XX
CC   The present invention describes a method for reducing viraemia or blood
CC   levels of a hepatitis virus antigen in an individual infected with
CC   hepatitis B virus (HBV). The method comprises administering a composition
CC   comprising a polynucleotide having an immunostimulatory sequence (ISS) to
CC   the individual, where the ISS comprises the sequence 5'-C, G-3', an HBV
CC   antigen is not administered in conjunction with administration of the
CC   composition, and where the composition is administered in an amount
CC   sufficient to reduce HBV viraemia or blood levels of a hepatitis virus
CC   antigen. ISS has virucide, anti-inflammatory and hepatotropic activities,
CC   and can be used in gene therapy. The method can be used for suppressing
CC   and/or ameliorating hepatitis infection in an individual, especially for
CC   preventing, palliating, ameliorating, reducing and/or eliminating one or
CC   more symptoms of HBV or HCV (hepatitis C virus) infection without
CC   administering HBV or HCV antigens. The method is specifically useful for
CC   reducing viraemia and hepatitis viral antigen in blood. ISS-containing
CC   polynucleotides may also be used to improve physical symptoms such as
CC   jaundice, fatigue, abdominal pain, and other clinical/ laboratory
CC   findings associated with hepatitis such as blood levels of liver enzymes,
CC   portal hypertension, or cirrhosis. The present sequence represents an ISS
CC   oligonucleotide given in the exemplification of the present invention
XX
SQ   Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             78.1%;  Score 16.4;  DB 6;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 72;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || ||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 28
```

```
ABL12595/c
ID   ABL12595 standard; cDNA; 1017 BP.
XX
AC   ABL12595;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 32267.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB68492.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 32267; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1017 BP; 246 A; 275 C; 290 G; 206 T; 0 U; 0 Other;

  Query Match             77.1%;  Score 16.2;  DB 4;  Length 1017;
  Best Local Similarity   85.7%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||||| | |||| ||||||
Db        253 TCGTCGAGCATTCGTGATGAT 233


RESULT 29
ACA47671
ID   ACA47671 standard; DNA; 1020 BP.
XX
AC   ACA47671;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #29328.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Staphylococcus haemolyticus.
XX
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PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU43801.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 35541; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1020 BP; 351 A; 148 C; 204 G; 317 T; 0 U; 0 Other;

Query Match 77.1%; Score 16.2; DB 7; Length 1020;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
|| ||| |||||||||||||
Db 922 TTGTGGAATGTTCGAGATGAT 942

RESULT 30
ABQ14749/c
ID ABQ14749 standard; DNA; 1676 BP.
XX
AC ABQ14749;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1340.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 1676 BP; 643 A; 513 C; 171 G; 349 T; 0 U; 0 Other;

Query Match 77.1%; Score 16.2; DB 6; Length 1676;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
|||| |||||||||||||
Db 1164 TCGTTAGACGTTCGAGATGAT 1144

RESULT 31
ABQ14748
ID ABQ14748 standard; DNA; 1676 BP.
XX
AC ABQ14748;
XX
DT 12-JUL-2002 (first entry)

XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1339.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 1676 BP; 349 A; 171 C; 513 G; 643 T; 0 U; 0 Other;

Query Match 77.1%; Score 16.2; DB 6; Length 1676;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||   ||||||||||||||
Db        513 TCGTTAGACGTTCGAGATGAT 533
```

RESULT 32
ABL12594
ID ABL12594 standard; cDNA; 3017 BP.
XX
AC ABL12594;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32264.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB68491.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 32264; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3017 BP; 808 A; 667 C; 672 G; 870 T; 0 U; 0 Other;

Query Match 77.1%; Score 16.2; DB 4; Length 3017;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||||| | |||| ||||||
Db       1765 TCGTCGAGCATTCGTGATGAT 1785
```

RESULT 33
ACA33960/c
ID ACA33960 standard; DNA; 3126 BP.
XX
AC ACA33960;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #15617.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Enterococcus faecium.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU30090.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 21830; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3126 BP; 1280 A; 536 C; 627 G; 683 T; 0 U; 0 Other;

Query Match 77.1%; Score 16.2; DB 7; Length 3126;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
|||| |||||| ||||||||
Db 2719 TCGTTAAACGTTGGAGATGAT 2699

RESULT 34
ADC91948/c
ID ADC91948 standard; DNA; 3135 BP.
XX
AC ADC91948;
XX
DT 01-JAN-2004 (first entry)
XX
DE E. faecium DNA sequence SEQ ID 1575.
XX
KW ds; gene; urinary tract infection; bacteraemia; endocarditis; wound;
KW abdominal-pelvic infection.
XX
OS Enterococcus faecium.
XX
PN US6583275-B1.
XX
PD 24-JUN-2003.
XX
PF 30-JUN-1998; 98US-00107532.
XX
PR 02-JUL-1997; 97US-0051571P.
PR 14-MAY-1998; 98US-0085598P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR WPI; 2003-799836/75.
DR P-PSDB; ADC95602.
XX
PT New isolated nucleic acid derived from Enterococcus faecium encoding an
PT Enterococcus faecium polypeptide useful for detection, prevention and
PT treatment of a pathological condition resulting from a bacterial
PT infection.
XX
PS Example 1; SEQ ID NO 1575; 243pp; English.
XX
CC The invention relates to an isolated nucleic acid derived from
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC one of 10 fully defined sequences given in the (or comprising 40
CC sequential nucleotides chosen from any of the nucleic acids, its
CC complement or sequences hybridising to it). Also included are a
CC recombinant vector comprising the nucleic acid operably linked to
CC transcription regulatory element, a cell comprising the vector and a
CC single-stranded probe comprising the nucleic acid. The nucleic acids are
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC The nucleic acids is useful for diagnosing pathological conditions
CC resulting from E. faecium bacterial infection (e.g. urinary tract
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC infection) and for screening drugs such as agonists and antagonists. The
CC nucleic acid is useful for recombinant production of Candida albicans -
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating Enterococcus faecium infections. The present sequence represents
CC one if the disclosed E. faecium nucleic acids.
XX
SQ Sequence 3135 BP; 1285 A; 537 C; 628 G; 685 T; 0 U; 0 Other;

Query Match 77.1%; Score 16.2; DB 9; Length 3135;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
|||| |||||| ||||||||
Db 2725 TCGTTAAACGTTGGAGATGAT 2705

RESULT 35
AAV17086/c
ID AAV17086 standard; cDNA; 4024 BP.
XX
AC AAV17086;
XX
DT 21-JUL-1998 (first entry)
XX
DE Bos taurus tubulin-folding cofactor D gene.
XX
KW Tubulin folding; cofactor; alpha-tubulin; beta-tubulin; unfolded; folded;
KW treatment; hyper-proliferative diseases; cancer; gout; ss.
XX
OS Bos taurus.
XX
FH Key Location/Qualifiers
FT CDS 192. .3791
FT /*tag= a

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FT                   /product= "bovine tubulin-folding cofactor D"
XX
PN   WO9804587-A1.
XX
PD   05-FEB-1998.
XX
PF   25-JUL-1997;   97WO-US014076.
XX
PR   25-JUL-1996;   96US-0023089P.
XX
PA   (UYNY ) UNIV NEW YORK STATE.
XX
PI   Cowan NJ;
XX
DR   WPI; 1998-130618/12.
DR   P-PSDB; AAW47206.
XX
PT   New isolated cofactor(s) for tubulin folding - are useful as targets for
PT   identifying agents which interfere with folding in the treatment of hyper
PT   -proliferative diseases such as cancer.
XX
PS   Claim 4; Page 57-61; 87pp; English.
XX
CC   The sequence is that encoding bovine tubulin-folding cofactor D which may
CC   be useful as a target for interfering with the production of productively
CC   folded alpha- and beta-tubulins. Since tubulin function is essential for
CC   cell division and proliferation, agents which interfere with tubulin
CC   function can serve as useful antiproliferative compounds. Such
CC   interfering agents have potential utility as agents for the treatment of
CC   hyperproliferative diseases such as cancer and the treatment of gout
XX
SQ   Sequence 4024 BP; 752 A; 1209 C; 1266 G; 797 T; 0 U; 0 Other;

  Query Match             77.1%;  Score 16.2;  DB 2;  Length 4024;
  Best Local Similarity   85.7%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              || |||||| || ||||||||
Db        557 TCCTCGAACCTTGGAGATGAT 537


RESULT 36
ADB88936
ID   ADB88936 standard; DNA; 66 BP.
XX
AC   ADB88936;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Chimeric immunomodulatory compound DNA sequence, SEQ ID No 139.
XX
KW   chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW   spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW   Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW   IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW   immunoglobulin E; IgE; allergy; cancer;
KW   stimulating cellular immune system cell; ss.
XX
OS   Synthetic.
XX
PN   WO2003000922-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US020025.
XX
PR   21-JUN-2001; 2001US-0299883P.
PR   23-APR-2002; 2002US-0375253P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D,  Tuck SF;
XX
DR   WPI; 2003-210159/20.
XX
PT   Novel chimeric immunomodulatory compound having immunomodulatory
PT   activity, useful for modulating an immune response and for treating
PT   cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS   Example 1; Page 110; 224pp; English.
XX
CC   The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC   having immunomodulatory activity, comprising two or more nucleic acid
CC   moieties and one or more non-nucleic acid spacer moieties, where at least
CC   one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC   acid moieties, where the spacer is not a polypeptide, and at least one
CC   nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC   immunodulatory compounds more specifically contain the nucleic acid
CC   spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC   CIC's are useful for modulating an immune response in an individual,
CC   where the individual suffers from a disorder associated with a Th2-type
CC   immune response which is an allergy or allergy-induced asthma, and an
CC   infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC   alpha; in an individual, where the individual has idiopathic pulmonary
CC   fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC   symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC   disorder in an individual, where the IgE-related disorder is allergy, or
CC   an allergy-related disorder. CIC's are also useful for treating cancer
CC   and can be used for stimulating cellular immune system cells production
CC   in an individual. This polynucleotide sequence represents a DNA sequence
CC   which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC   of the invention.
XX
SQ   Sequence 66 BP; 18 A; 9 C; 21 G; 18 T; 0 U; 0 Other;

  Query Match             76.2%;  Score 16;  DB 8;  Length 66;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGAT 21
              ||||||||||||||||
Db          8 GAACGTTCGAGATGAT 23


RESULT 37
ABQ75223
ID   ABQ75223 standard; DNA; 19 BP.
XX
AC   ABQ75223;
XX
DT   05-NOV-2002  (first entry)
XX
DE   ISS immunomodulatory oligonucleotide SEQ ID NO:58.
XX
KW   Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW   allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW   idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW   malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW   immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW   virucide; antibacterial; protozoacide; ss.
XX
OS   Synthetic.
XX
PN   WO200252002-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-US050821.
XX
PR   27-DEC-2000; 2000US-0258675P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Fearon KL,  Dina D;
XX
```

DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence.
XX
PS Disclosure; Page 22; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from the
CC present invention
XX
SQ Sequence 19 BP; 2 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 75.2%; Score 15.8; DB 6; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
|||||| ||||||||||
Db 1 TCGTCGTTCGTTCGAGATG 19

RESULT 38
ADB88893
ID ADB88893 standard; DNA; 19 BP.
XX
AC ADB88893;
XX
DT 04-DEC-2003 (first entry)
XX
DE Chimeric immunomodulatory compound DNA sequence, SEQ ID No 96.
XX
KW chimeric immunomodulatory compound; CIC; immunomodulatory activity;
KW spacer moiety; linear hexaethylene glycol structure; HEG; immune;
KW Th2-type; allergy; allergy-induced asthma; infectious disease; IFN-gamma;
KW IFN-alpha; idiopathic pulmonary fibrosis; viral infection; ameliorating;
KW immunoglobulin E; IgE; allergy; cancer;
KW stimulating cellular immune system cell; ss.
XX
OS Synthetic.
XX
PN WO2003000922-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US020025.
XX
PR 21-JUN-2001; 2001US-0299883P.
PR 23-APR-2002; 2002US-0375253P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D, Tuck SF;
XX

DR WPI; 2003-210159/20.
XX
PT Novel chimeric immunomodulatory compound having immunomodulatory
PT activity, useful for modulating an immune response and for treating
PT cancer, has nucleic acid moieties and non-nucleic acid spacer moieties.
XX
PS Disclosure; Page 35; 224pp; English.
XX
CC The invention relates to a novel chimeric immunomodulatory compound (CIC)
CC having immunomodulatory activity, comprising two or more nucleic acid
CC moieties and one or more non-nucleic acid spacer moieties, where at least
CC one non-nucleic acid spacer moiety is covalently joined to two nucleic
CC acid moieties, where the spacer is not a polypeptide, and at least one
CC nucleic acid moiety comprises the sequence 5'-CG-3'. The chimeric
CC immunodulatory compounds more specifically contain the nucleic acid
CC spacer moieties of linear hexaethylene glycol structure (HEG) subunits.
CC CIC's are useful for modulating an immune response in an individual,
CC where the individual suffers from a disorder associated with a Th2-type
CC immune response which is an allergy or allergy-induced asthma, and an
CC infectious disease. CIC is also useful for increasing IFN-gamma;, or IFN-
CC alpha; in an individual, where the individual has idiopathic pulmonary
CC fibrosis, or a viral infection. CIC's are useful for ameliorating a
CC symptom of an infectious disease, or an immunoglobulin E (IgE)-related
CC disorder in an individual, where the IgE-related disorder is allergy, or
CC an allergy-related disorder. CIC's are also useful for treating cancer
CC and can be used for stimulating cellular immune system cells production
CC in an individual. This polynucleotide sequence represents a DNA sequence
CC which is a nucleic acid moiety part of a chimeric immunodulatory compound
CC of the invention.
XX
SQ Sequence 19 BP; 2 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 75.2%; Score 15.8; DB 8; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
|||||| ||||||||||
Db 1 TCGTCGTTCGTTCGAGATG 19

RESULT 39
ABL09441/c
ID ABL09441 standard; cDNA; 2726 BP.
XX
AC ABL09441;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22805.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB65338.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 22805; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2726 BP; 659 A; 657 C; 781 G; 629 T; 0 U; 0 Other;

Query Match 75.2%; Score 15.8; DB 4; Length 2726;
Best Local Similarity 89.5%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GTCGAACGTTCGAGATGAT 21
||||||||| ||| ||||||
Db 155 GTCGAACGATCGTGATGAT 137

RESULT 40
ABL09440/c
ID ABL09440 standard; cDNA; 5080 BP.
XX
AC ABL09440;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22802.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB65337.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 22802; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 5080 BP; 1302 A; 1201 C; 1301 G; 1276 T; 0 U; 0 Other;

Query Match 75.2%; Score 15.8; DB 4; Length 5080;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GTCGAACGTTCGAGATGAT 21
||||||||| ||| ||||||
Db 1155 GTCGAACGATCGTGATGAT 1137

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Job time : 401 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Searched: 2470430 seqs, 1873665578 residues

Total number of hits satisfying chosen parameters: 4940860

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	21	14	US-10-033-243-132	Sequence 132, App
2	19	90.5	19	10	US-09-927-422A-16	Sequence 16, Appl
3	19	90.5	19	14	US-10-033-243-19	Sequence 19, Appl
4	19	90.5	19	14	US-10-176-883-41	Sequence 41, Appl
5	19	90.5	19	14	US-10-177-826-41	Sequence 41, Appl
6	19	90.5	22	14	US-10-033-243-30	Sequence 30, Appl
7	19	90.5	22	14	US-10-176-883-52	Sequence 52, Appl
8	19	90.5	22	14	US-10-177-826-52	Sequence 52, Appl
9	18	85.7	19	14	US-10-033-243-24	Sequence 24, Appl
10	18	85.7	19	14	US-10-176-883-46	Sequence 46, Appl
11	18	85.7	19	14	US-10-177-826-46	Sequence 46, Appl
12	17.4	82.9	19	14	US-10-033-243-56	Sequence 56, Appl
13	17.4	82.9	19	14	US-10-033-243-57	Sequence 57, Appl
14	17.4	82.9	19	14	US-10-176-883-94	Sequence 94, Appl
15	17.4	82.9	19	14	US-10-176-883-95	Sequence 95, Appl
16	17.4	82.9	19	14	US-10-177-826-94	Sequence 94, Appl
17	17.4	82.9	19	14	US-10-177-826-95	Sequence 95, Appl
18	17	81.0	19	14	US-10-033-243-23	Sequence 23, Appl
19	17	81.0	19	14	US-10-176-883-45	Sequence 45, Appl
20	17	81.0	19	14	US-10-177-826-45	Sequence 45, Appl
21	16.4	78.1	18	14	US-10-033-243-14	Sequence 14, Appl
22	16.4	78.1	18	14	US-10-176-883-36	Sequence 36, Appl
23	16.4	78.1	18	14	US-10-177-826-36	Sequence 36, Appl
c 24	16.4	78.1	23	9	US-09-802-686-3	Sequence 3, Appli
c 25	16.4	78.1	23	9	US-09-802-685-3	Sequence 3, Appli
c 26	16.4	78.1	23	9	US-09-802-376-3	Sequence 3, Appli
c 27	16.4	78.1	23	9	US-09-802-370-3	Sequence 3, Appli
c 28	16.4	78.1	23	9	US-09-802-445-3	Sequence 3, Appli
c 29	16.4	78.1	23	10	US-09-927-422A-3	Sequence 3, Appli
c 30	16.4	78.1	23	10	US-09-927-884-3	Sequence 3, Appli
c 31	16.4	78.1	23	10	US-09-802-359-3	Sequence 3, Appli
c 32	16.4	78.1	23	15	US-10-357-760-3	Sequence 3, Appli
c 33	16.4	78.1	23	15	US-10-413-504-4	Sequence 4, Appli
c 34	16.4	78.1	23	15	US-10-426-237-3	Sequence 3, Appli
c 35	16.4	78.1	450	12	US-10-424-599-21073	Sequence 21073, A
36	16.2	77.1	1020	12	US-10-282-122A-35541	Sequence 35541, A
c 37	16.2	77.1	3126	12	US-10-282-122A-21830	Sequence 21830, A
c 38	16.2	77.1	3999	12	US-10-424-599-28340	Sequence 28340, A
39	16	76.2	66	14	US-10-176-883-139	Sequence 139, App
40	16	76.2	66	14	US-10-177-826-139	Sequence 139, App
c 41	16	76.2	227	12	US-10-424-599-26981	Sequence 26981, A
42	15.8	75.2	19	14	US-10-033-243-58	Sequence 58, Appl
43	15.8	75.2	19	14	US-10-176-883-96	Sequence 96, Appl
44	15.8	75.2	19	14	US-10-177-826-96	Sequence 96, Appl
c 45	15.8	75.2	634	15	US-10-260-238-5181	Sequence 5181, Ap

ALIGNMENTS

RESULT 1
US-10-033-243-132
; Sequence 132, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; FILE REFERENCE: 377882001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-132

Query Match 100.0%; Score 21; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TCGTCGAACGTTCGAGATGAT 21
              |||||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATGAT 21
```

RESULT 2
US-09-927-422A-16
; Sequence 16, Application US/09927422A
; Publication No. US20030022852A1
; GENERAL INFORMATION:

```
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  APPLICANT:  Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  TITLE OF INVENTION: BIODEGRADABLE IMMUNOMODULATORY
;  TITLE OF INVENTION:  FORMULATIONS AND METHODS FOR USE THEREOF
;  FILE REFERENCE: 377882001420
;  CURRENT APPLICATION NUMBER: US/09/927,422A
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/802,359
;  PRIOR FILING DATE: 2001-03-09
;  PRIOR APPLICATION NUMBER: U.S. 60/188,30
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-927-422A-16

  Query Match             90.5%;  Score 19;  DB 10;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 3
US-10-033-243-19
; Sequence 19, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-19

  Query Match             90.5%;  Score 19;  DB 14;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 4
US-10-176-883-41
; Sequence 41, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-41

  Query Match             90.5%;  Score 19;  DB 14;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 5
US-10-177-826-41
; Sequence 41, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-II
;  FILE REFERENCE: 377882002001
;  CURRENT APPLICATION NUMBER: US/10/177,826
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-177-826-41

  Query Match             90.5%;  Score 19;  DB 14;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 6
US-10-033-243-30
; Sequence 30, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
```

; FILE REFERENCE: 377882001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-30

Query Match 90.5%; Score 19; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||||||||||||||||
Db 4 TCGTCGAACGTTCGAGATG 22

RESULT 7
US-10-176-883-52
; Sequence 52, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-I
; FILE REFERENCE: 377882002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-176-883-52

Query Match 90.5%; Score 19; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||||||||||||||||
Db 4 TCGTCGAACGTTCGAGATG 22

RESULT 8
US-10-177-826-52
; Sequence 52, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-II
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-52

Query Match 90.5%; Score 19; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||||||||||||||||
Db 4 TCGTCGAACGTTCGAGATG 22

RESULT 9
US-10-033-243-24
; Sequence 24, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; FILE REFERENCE: 377882001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5
; OTHER INFORMATION: n = 5-bromocytosine
US-10-033-243-24

Query Match 85.7%; Score 18; DB 14; Length 19;
Best Local Similarity 94.7%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
|||| ||||||||||||||
Db 1 TCGTNGAACGTTCGAGATG 19

RESULT 10
US-10-176-883-46
; Sequence 46, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-I
; FILE REFERENCE: 377882002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; CURRENT FILING DATE: 2002-06-21

```
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: variation
;   LOCATION: 5
;   OTHER INFORMATION: n = 5-bromocytosine
US-10-176-883-46

  Query Match             85.7%;  Score 18;  DB 14;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 13;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||| ||||||||||||||
Db          1 TCGTNGAACGTTCGAGATG 19


RESULT 11
US-10-177-826-46
; Sequence 46, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-II
;  FILE REFERENCE: 377882002001
;  CURRENT APPLICATION NUMBER: US/10/177,826
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: variation
;   LOCATION: 5
;   OTHER INFORMATION: n = 5-bromocytosine
US-10-177-826-46

  Query Match             85.7%;  Score 18;  DB 14;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 13;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||| ||||||||||||||
Db          1 TCGTNGAACGTTCGAGATG 19


RESULT 12
US-10-033-243-56
; Sequence 56, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-56

  Query Match             82.9%;  Score 17.4;  DB 14;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||| ||||||||||||
Db          1 TCGTCGGACGTTCGAGATG 19


RESULT 13
US-10-033-243-57
; Sequence 57, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-57

  Query Match             82.9%;  Score 17.4;  DB 14;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||| ||||||||||||
Db          1 TCGTCGTACGTTCGAGATG 19


RESULT 14
US-10-176-883-94
; Sequence 94, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
```

```
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-94

  Query Match             82.9%;  Score 17.4;  DB 14;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||| ||||||||||||
Db          1 TCGTCGGACGTTCGAGATG 19


RESULT 15
US-10-176-883-95
; Sequence 95, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-95

  Query Match             82.9%;  Score 17.4;  DB 14;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||| ||||||||||||
Db          1 TCGTCGTACGTTCGAGATG 19


RESULT 16
US-10-177-826-94
; Sequence 94, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-II
;  FILE REFERENCE: 377882002001
;  CURRENT APPLICATION NUMBER: US/10/177,826
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-177-826-94

  Query Match             82.9%;  Score 17.4;  DB 14;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||| ||||||||||||
Db          1 TCGTCGGACGTTCGAGATG 19


RESULT 17
US-10-177-826-95
; Sequence 95, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-II
;  FILE REFERENCE: 377882002001
;  CURRENT APPLICATION NUMBER: US/10/177,826
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-177-826-95

  Query Match             82.9%;  Score 17.4;  DB 14;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||| ||||||||||||
Db          1 TCGTCGTACGTTCGAGATG 19


RESULT 18
US-10-033-243-23
; Sequence 23, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2, 5
;   OTHER INFORMATION: n = 5-bromocytocine
US-10-033-243-23

  Query Match             81.0%;  Score 17;  DB 14;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 42;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              | || ||||||||||||||||
Db          1 TNGTNGAACGTTCGAGATG 19


RESULT 19
US-10-176-883-45
; Sequence 45, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: variation
;   LOCATION: 2, 5
;   OTHER INFORMATION: n = 5-bromocytosine
US-10-176-883-45

  Query Match             81.0%;  Score 17;  DB 14;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 42;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              | || ||||||||||||||||
Db          1 TNGTNGAACGTTCGAGATG 19


RESULT 20
US-10-177-826-45
; Sequence 45, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-II
;  FILE REFERENCE: 377882002001
;  CURRENT APPLICATION NUMBER: US/10/177,826
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: variation
;   LOCATION: 2, 5
;   OTHER INFORMATION: n = 5-bromocytosine
US-10-177-826-45

  Query Match             81.0%;  Score 17;  DB 14;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 42;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              | || ||||||||||||||||
Db          1 TNGTNGAACGTTCGAGATG 19


RESULT 21
US-10-033-243-14
; Sequence 14, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-14

  Query Match             78.1%;  Score 16.4;  DB 14;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 87;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATG 19
              | ||||||||||||||||||
Db          1 CTTCGAACGTTCGAGATG 18


RESULT 22
US-10-176-883-36
; Sequence 36, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
```

```
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-36

  Query Match             78.1%;  Score 16.4;  DB 14;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 87;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATG 19
              | ||||||||||||||||
Db          1 CTTCGAACGTTCGAGATG 18


RESULT 23
US-10-177-826-36
; Sequence 36, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-II
;  FILE REFERENCE: 377882002001
;  CURRENT APPLICATION NUMBER: US/10/177,826
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-177-826-36

  Query Match             78.1%;  Score 16.4;  DB 14;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 87;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATG 19
              | ||||||||||||||||
Db          1 CTTCGAACGTTCGAGATG 18


RESULT 24
US-09-802-686-3/c
; Sequence 3, Application US/09802686
; Patent No. US20010046967A1
; GENERAL INFORMATION:
;  APPLICANT: Dynavax Technologies Corporation
;  APPLICANT:  Van Nest, Gary
;  TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING
;  TITLE OF INVENTION:  RESPIRATORY VIRAL INFECTION USING IMMUNOMODULATORY
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 377882000900
;  CURRENT APPLICATION NUMBER: US/09/802,686
;  CURRENT FILING DATE:  2001-03-09
;  PRIOR APPLICATION NUMBER: 60/188,583
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-686-3

  Query Match             78.1%;  Score 16.4;  DB 9;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || ||||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 25
US-09-802-685-3/c
; Sequence 3, Application US/09802685
; Patent No. US20020028784A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Eiden, Joseph J., Jr.
;  TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING VIRAL
;  TITLE OF INVENTION:  INFECTIONS USING IMMUNOMODULATORY POLYNUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 377882001600
;  CURRENT APPLICATION NUMBER: US/09/802,685
;  CURRENT FILING DATE:  2001-03-09
;  PRIOR APPLICATION NUMBER: U.S. 60/188,302
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-685-3

  Query Match             78.1%;  Score 16.4;  DB 9;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || ||||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 26
US-09-802-376-3/c
; Sequence 3, Application US/09802376
; Patent No. US20020055477A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
;  FILE REFERENCE: 37788201700
;  CURRENT APPLICATION NUMBER: US/09/802,376
;  CURRENT FILING DATE:  2001-03-09
;  PRIOR APPLICATION NUMBER: 60/188,557
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 23
;   TYPE: DNA
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-3

  Query Match             78.1%;  Score 16.4;  DB 9;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 27
US-09-802-370-3/c
; Sequence 3, Application US/09802370
; Patent No. US20020098199A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Eiden, Joseph J. Jr.
;  TITLE OF INVENTION: METHODS OF SUPPRESSING HEPATITIS VIRUS
;  TITLE OF INVENTION:  INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 377882001200
;  CURRENT APPLICATION NUMBER: US/09/802,370
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: 60/188,301
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-370-3

  Query Match             78.1%;  Score 16.4;  DB 9;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 28
US-09-802-445-3/c
; Sequence 3, Application US/09802445
; Patent No. US20020107212A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Eiden, Joseph J. Jr.
;  TITLE OF INVENTION: METHODS OF REDUCING PAPILLOMAVIRUS INFECTION USING IMMUNOMODULATC
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 377882001300
;  CURRENT APPLICATION NUMBER: US/09/802,445
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: 60/188,265
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-445-3

  Query Match             78.1%;  Score 16.4;  DB 9;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 29
US-09-927-422A-3/c
; Sequence 3, Application US/09927422A
; Publication No. US20030022852A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  APPLICANT:  Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  TITLE OF INVENTION: BIODEGRADABLE IMMUNOMODULATORY
;  TITLE OF INVENTION:  FORMULATIONS AND METHODS FOR USE THEREOF
;  FILE REFERENCE: 377882001420
;  CURRENT APPLICATION NUMBER: US/09/927,422A
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/802,359
;  PRIOR FILING DATE: 2001-03-09
;  PRIOR APPLICATION NUMBER: U.S. 60/188,30
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-927-422A-3

  Query Match             78.1%;  Score 16.4;  DB 10;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1


RESULT 30
US-09-927-884-3/c
; Sequence 3, Application US/09927884
; Publication No. US20030059773A1
; GENERAL INFORMATION:
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  APPLICANT:  Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND
;  TITLE OF INVENTION:  METHODS FOR USE THEREOF
;  FILE REFERENCE: 377882001720
;  CURRENT APPLICATION NUMBER: US/09/927,884
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/802,376
;  PRIOR FILING DATE: 2001-03-09
;  PRIOR APPLICATION NUMBER: U.S. 60/188,557
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-927-884-3

  Query Match             78.1%;  Score 16.4;  DB 10;  Length 23;
```

Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 GTCGAACGTTCGAGATGA 20
              || ||||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1
```

RESULT 31
US-09-802-359-3/c
; Sequence 3, Application US/09802359
; Publication No. US20030129251A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-3

Query Match 78.1%; Score 16.4; DB 10; Length 23;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 GTCGAACGTTCGAGATGA 20
              || ||||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1
```

RESULT 32
US-10-357-760-3/c
; Sequence 3, Application US/10357760
; Publication No. US20030216340A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Eiden, Joseph J. Jr.
; TITLE OF INVENTION: METHODS OF SUPPRESSING HEPATITIS VIRUS
; TITLE OF INVENTION: INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE SEQUENCES
; FILE REFERENCE: 377882001200
; CURRENT APPLICATION NUMBER: US/10/357,760
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/802,370
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/188,301
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-357-760-3

Query Match 78.1%; Score 16.4; DB 15; Length 23;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 GTCGAACGTTCGAGATGA 20
              || ||||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1
```

RESULT 33
US-10-413-504-4/c
; Sequence 4, Application US/10413504
; Publication No. US20040006034A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Schwartz, David
; APPLICANT: Roman, Mark
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE THEREOF
; FILE REFERENCE: 37788-20004.01
; CURRENT APPLICATION NUMBER: US/10/413,504
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 09/296,477
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 09/092,329
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunostimulatory oligonucleotide
US-10-413-504-4

Query Match 78.1%; Score 16.4; DB 15; Length 23;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 GTCGAACGTTCGAGATGA 20
              || ||||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1
```

RESULT 34
US-10-426-237-3/c
; Sequence 3, Application US/10426237
; Publication No. US20040009942A1
; GENERAL INFORMATION:
; APPLICANT: Dynavax Technologies Corporation
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING
; TITLE OF INVENTION: RESPIRATORY VIRAL INFECTION USING IMMUNOMODULATORY
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES
; FILE REFERENCE: 377882000920
; CURRENT APPLICATION NUMBER: US/10/426,237
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 09/802,686
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,583
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-426-237-3

Query Match 78.1%; Score 16.4; DB 15; Length 23;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 GTCGAACGTTCGAGATGA 20
              || ||||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1
```

```
RESULT 35
US-10-424-599-21073/c
; Sequence 21073, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 21073
;   LENGTH: 450
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_119033C.1
US-10-424-599-21073

  Query Match             78.1%;  Score 16.4;  DB 12;  Length 450;
  Best Local Similarity   94.4%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATGAT 21
              ||||| ||||||||||||
Db        373 TCGAATGTTCGAGATGAT 356


RESULT 36
US-10-282-122A-35541
; Sequence 35541, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35541
;   LENGTH: 1020
;   TYPE: DNA
;   ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-35541

  Query Match             77.1%;  Score 16.2;  DB 12;  Length 1020;
  Best Local Similarity   85.7%;  Pred. No. 1.4e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              | || ||| ||||||||||||
Db        922 TTGTGGAATGTTCGAGATGAT 942


RESULT 37
US-10-282-122A-21830/c
; Sequence 21830, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21830
;   LENGTH: 3126
;   TYPE: DNA
;   ORGANISM: Enterococcus faecium
US-10-282-122A-21830

  Query Match             77.1%;  Score 16.2;  DB 12;  Length 3126;
  Best Local Similarity   85.7%;  Pred. No. 1.5e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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```
Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||  ||||||  ||||||||
Db       2719 TCGTTAAACGTTGGAGATGAT 2699


RESULT 38
US-10-424-599-28340/c
; Sequence 28340, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 28340
;   LENGTH: 3999
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_125592C.1
US-10-424-599-28340

  Query Match             77.1%;  Score 16.2;  DB 12;  Length 3999;
  Best Local Similarity   85.7%;  Pred. No. 1.6e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              || ||||||  ||||||||| |
Db       1863 TCCTCGAACTTTCGAGATGGT 1843


RESULT 39
US-10-176-883-139
; Sequence 139, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 139
;   LENGTH: 66
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-139

  Query Match             76.2%;  Score 16;  DB 14;  Length 66;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGAT 21
              ||||||||||||||||
Db          8 GAACGTTCGAGATGAT 23


RESULT 40
US-10-177-826-139
; Sequence 139, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-II
;  FILE REFERENCE: 377882002001
;  CURRENT APPLICATION NUMBER: US/10/177,826
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 139
;   LENGTH: 66
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-177-826-139

  Query Match             76.2%;  Score 16;  DB 14;  Length 66;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGAT 21
              ||||||||||||||||
Db          8 GAACGTTCGAGATGAT 23


Search completed: April  6, 2004, 04:04:03
Job time : 346 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 6, 2004, 01:41:36 ; Search time 75 Seconds
(without alignments)
155.386 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgtcgaacgttcgagatgat 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	16.4	78.1	23	4	US-09-296-477-4	Sequence 4, Appli
c	2	16.2	77.1	3135	4	US-09-107-532A-1575	Sequence 1575, Ap
	3	15.4	73.3	816	3	US-08-776-251-10	Sequence 10, Appl
c	4	15.4	73.3	816	3	US-08-776-251-10	Sequence 10, Appl
c	5	15.4	73.3	1900	4	US-09-555-000-1	Sequence 1, Appli
	6	15.2	72.4	342	4	US-09-134-000C-2551	Sequence 2551, Ap
c	7	15.2	72.4	4590	4	US-09-134-001C-1108	Sequence 1108, Ap
	8	15.2	72.4	10619	4	US-10-204-708-4	Sequence 4, Appli
	9	15	71.4	22	4	US-09-235-742-19	Sequence 19, Appl
	10	15	71.4	22	4	US-09-347-343-32	Sequence 32, Appl
	11	15	71.4	22	4	US-09-820-484-1	Sequence 1, Appli
	12	15	71.4	22	4	US-09-820-484-3	Sequence 3, Appli
	13	15	71.4	22	4	US-09-774-403A-1	Sequence 1, Appli
	14	15	71.4	22	4	US-09-296-477-1	Sequence 1, Appli
	15	15	71.4	22	4	US-09-296-477-2	Sequence 2, Appli
c	16	15	71.4	22	4	US-09-296-477-5	Sequence 5, Appli
	17	15	71.4	22	4	US-09-308-036A-1	Sequence 1, Appli
	18	15	71.4	22	4	US-09-791-500-1	Sequence 1, Appli
	19	14.8	70.5	813	4	US-09-107-532A-1566	Sequence 1566, Ap
	20	14.8	70.5	1069	4	US-09-374-174B-1	Sequence 1, Appli
	21	14.8	70.5	1497	4	US-09-252-991A-2256	Sequence 2256, Ap
c	22	14.8	70.5	1950	4	US-09-252-991A-2425	Sequence 2425, Ap
	23	14.8	70.5	2799	1	US-08-446-794A-5	Sequence 5, Appli
	24	14.8	70.5	2799	1	US-08-750-007-4	Sequence 4, Appli
	25	14.6	69.5	424	4	US-09-621-976-12664	Sequence 12664, A
	26	14.6	69.5	3468	4	US-09-221-017B-893	Sequence 893, App
	27	14.4	68.6	77	1	US-08-399-412A-58	Sequence 58, Appl
	28	14.2	67.6	77	1	US-08-447-169A-36	Sequence 36, Appl
	29	14.2	67.6	77	2	US-08-233-012C-36	Sequence 36, Appl
	30	14.2	67.6	1535	4	US-09-848-295-1	Sequence 1, Appli
	31	14.2	67.6	4715	4	US-08-956-171E-203	Sequence 203, App
c	32	14.2	67.6	14636	3	US-09-173-914-6	Sequence 6, Appli
c	33	14.2	67.6	50937	3	US-09-428-517-1	Sequence 1, Appli
c	34	14.2	67.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	35	14.2	67.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	36	14	66.7	22	4	US-09-296-477-15	Sequence 15, Appl
c	37	13.8	65.7	66	2	US-08-710-134-63	Sequence 63, Appl
c	38	13.8	65.7	66	2	US-08-485-885-63	Sequence 63, Appl
c	39	13.8	65.7	86	2	US-08-710-134-64	Sequence 64, Appl
c	40	13.8	65.7	86	2	US-08-485-885-64	Sequence 64, Appl
	41	13.8	65.7	173	4	US-09-313-294A-3045	Sequence 3045, Ap
c	42	13.8	65.7	223	4	US-08-956-171E-1271	Sequence 1271, Ap
c	43	13.8	65.7	321	3	US-09-240-274-197	Sequence 197, App
	44	13.8	65.7	459	4	US-09-540-236-1391	Sequence 1391, Ap
c	45	13.8	65.7	531	4	US-09-134-000C-1500	Sequence 1500, Ap

ALIGNMENTS

RESULT 1
US-09-296-477-4/c
; Sequence 4, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-296-477-4

Query Match 78.1%; Score 16.4; DB 4; Length 23;
Best Local Similarity 94.4%; Pred. No. 5.5;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 GTCGAACGTTCGAGATGA 20
              || |||||||||||||||
Db         18 GTGGAACGTTCGAGATGA 1
```

RESULT 2
US-09-107-532A-1575/c
; Sequence 1575, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street

```
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;          COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;          CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;          PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;          ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;          TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;       INFORMATION FOR SEQ ID NO: 1575:
;          SEQUENCE CHARACTERISTICS:
;             LENGTH: 3135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;          MOLECULE TYPE: DNA (genomic)
;          HYPOTHETICAL: NO
;          ANTI-SENSE: NO
;          ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;          FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...3135
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1575:
US-09-107-532A-1575

  Query Match             77.1%;  Score 16.2;  DB 4;  Length 3135;
  Best Local Similarity   85.7%;  Pred. No. 13;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||  ||||||  ||||||||
Db       2725 TCGTTAAACGTTGGAGATGAT 2705


RESULT 3
US-08-776-251-10
; Sequence 10, Application US/08776251
; Patent No. 6025340
;  GENERAL INFORMATION:
;     APPLICANT:  Springer, Caroline J
;     APPLICANT:  Marais, Richard
;     TITLE OF INVENTION:  Surface expression of enzyme in gene directed prodrug therapy
;     NUMBER OF SEQUENCES:  27
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Nixon & Vanderhye
;       STREET:  1100 No. 6025340th Glebe Road, 8th Floor
;       CITY:  Arlington
;       STATE:  Virginia
;       COUNTRY:  USA
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/776,251
;       FILING DATE:  31-JAN-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/GB95/01782
;       FILING DATE:  27-JUL-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9415167.7
;       FILING DATE:  27-JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Arthur R. Crawford
;       REGISTRATION NUMBER:  25,327
;       REFERENCE/DOCKET NUMBER:  620-20
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  816 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-776-251-10

  Query Match             73.3%;  Score 15.4;  DB 3;  Length 816;
  Best Local Similarity   94.1%;  Pred. No. 31;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATGA 20
              |||||||||||||| ||
Db        619 TCGAACGTTCGAGACGA 635


RESULT 4
US-08-776-251-10/c
; Sequence 10, Application US/08776251
; Patent No. 6025340
;  GENERAL INFORMATION:
;     APPLICANT:  Springer, Caroline J
;     APPLICANT:  Marais, Richard
;     TITLE OF INVENTION:  Surface expression of enzyme in gene directed prodrug therapy
;     NUMBER OF SEQUENCES:  27
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Nixon & Vanderhye
;       STREET:  1100 No. 6025340th Glebe Road, 8th Floor
;       CITY:  Arlington
;       STATE:  Virginia
;       COUNTRY:  USA
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/776,251
;       FILING DATE:  31-JAN-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/GB95/01782
;       FILING DATE:  27-JUL-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9415167.7
;       FILING DATE:  27-JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Arthur R. Crawford
;       REGISTRATION NUMBER:  25,327
;       REFERENCE/DOCKET NUMBER:  620-20
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  816 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-776-251-10

  Query Match             73.3%;  Score 15.4;  DB 3;  Length 816;
  Best Local Similarity   94.1%;  Pred. No. 31;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          4 TCGAACGTTCGAGATGA 20
              ||||||||||||||| ||
Db        630 TCGAACGTTCGAGACGA 614


RESULT 5
US-09-555-000-1/c
; Sequence 1, Application US/09555000
; Patent No. 6489108
; GENERAL INFORMATION:
;  APPLICANT:  Genencor International, Inc.
;  TITLE OF INVENTION:  Proteases from Gram Positive Organisms
;  FILE REFERENCE:  GC390-PCT
;  CURRENT APPLICATION NUMBER: US/09/555,000
;  CURRENT FILING DATE:  2000-05-23
;  PRIOR APPLICATION NUMBER:  PCT/US98/26971
;  PRIOR FILING DATE:  1998-12-17
;  NUMBER OF SEQ ID NOS:  2
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1900
;   TYPE: DNA
;   ORGANISM: Bacillus subtilis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (134)...(1774)
US-09-555-000-1

  Query Match             73.3%;  Score 15.4;  DB 4;  Length 1900;
  Best Local Similarity   94.1%;  Pred. No. 34;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CGAACGTTCGAGATGAT 21
              |||||||||||  |||||
Db       1119 CGAACGTTCGACATGAT 1103


RESULT 6
US-09-134-000C-2551
; Sequence 2551, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2551
;   LENGTH: 342
;   TYPE: DNA
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-2551

  Query Match             72.4%;  Score 15.2;  DB 4;  Length 342;
  Best Local Similarity   85.0%;  Pred. No. 36;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGA 20
              ||||||||  ||||  |||||
Db         31 TCGTCGAAGGTTCCTGATGA 50


RESULT 7
US-09-134-001C-1108/c
; Sequence 1108, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1108
;   LENGTH: 4590
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1108

  Query Match             72.4%;  Score 15.2;  DB 4;  Length 4590;
  Best Local Similarity   85.0%;  Pred. No. 50;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||||  ||| |||
Db       3597 CGTCGAACGTTGAAGAAGAT 3578


RESULT 8
US-10-204-708-4
; Sequence 4, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
;  TITLE OF INVENTION:  by Assessing DNA Methylation
;  FILE REFERENCE: 5013.1012
;  CURRENT APPLICATION NUMBER: US/10/204,708
;  CURRENT FILING DATE:  2003-05-06
;  PRIOR APPLICATION NUMBER: PCT/EP01/03971
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: DE 10019058.8
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
;   LENGTH: 10619
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-4

  Query Match             72.4%;  Score 15.2;  DB 4;  Length 10619;
  Best Local Similarity   85.0%;  Pred. No. 55;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||| ||| ||||| ||||||
Db       9684 CGTAGAATGTTCGTGATGAT 9703


RESULT 9
US-09-235-742-19
; Sequence 19, Application US/09235742
; Patent No. 6498148
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
```

```
;  TITLE OF INVENTION: Immunization-Free Methods for Treating
;  TITLE OF INVENTION: Antigen-Stimulated Inflammation in a Mammalian Host and
;  TITLE OF INVENTION: Shifting the Host's Antigen Immune Responsiveness to a TH1
;  TITLE OF INVENTION: Phenotype
;  FILE REFERENCE: 6510-170CON4
;  CURRENT APPLICATION NUMBER: US/09/235,742
;  CURRENT FILING DATE: 1999-01-21
;  EARLIER APPLICATION NUMBER: 08/927,120
;  EARLIER FILING DATE: 1997-09-05
;  EARLIER APPLICATION NUMBER: 08/593,554
;  EARLIER FILING DATE: 1996-01-30
;  EARLIER APPLICATION NUMBER: 08/725,968
;  EARLIER FILING DATE: 1996-10-04
;  EARLIER APPLICATION NUMBER: 60/028,118
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant or Synthetic Sequence
US-09-235-742-19

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 10
US-09-347-343-32
; Sequence 32, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
;  APPLICANT: RAZ, Eyal R.
;  APPLICANT: KOBAYASHI, Hiroko
;  TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
;  FILE REFERENCE: 30448.64US01
;  CURRENT APPLICATION NUMBER: US/09/347,343A
;  CURRENT FILING DATE: 1999-07-02
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: synthetic oligonucleotide
US-09-347-343-32

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 11
US-09-820-484-1
; Sequence 1, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
;   NAME/KEY: modified_base
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: disulfide thymine
US-09-820-484-1

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 12
US-09-820-484-3
; Sequence 3, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: phosphorothioate ISS-ODN
US-09-820-484-3

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 13
US-09-774-403A-1
; Sequence 1, Application US/09774403A
```

```
; Patent No. 6552006
; GENERAL INFORMATION:
;  APPLICANT: Eyal Raz
;  APPLICANT:  Richard Kornbluth
;  APPLICANT:  Antonio Catanzaro
;  APPLICANT:  Tomoko Hayashi
;  APPLICANT:  Dennis Carson
;  TITLE OF INVENTION: Immunomodulatory Polynucleotides in
;  TITLE OF INVENTION:  Treatment of Infection by an Intracellular Pathogen
;  FILE REFERENCE: UCAL166
;  CURRENT APPLICATION NUMBER: US/09/774,403A
;  CURRENT FILING DATE:  2002-04-15
;  PRIOR APPLICATION NUMBER: 60/179,353
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Immunomodulatory sequence
US-09-774-403A-1

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 14
US-09-296-477-1
; Sequence 1, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-296-477-1

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 15
US-09-296-477-2
; Sequence 2, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-296-477-2

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 16
US-09-296-477-5/c
; Sequence 5, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-296-477-5

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db         15 GAACGTTCGAGATGA 1
```

```
RESULT 17
US-09-308-036A-1
; Sequence 1, Application US/09308036A
; Patent No. 6610661
; GENERAL INFORMATION:
;  APPLICANT: Carson, Dennis A.
;  APPLICANT:  Raz, Eyal
;  APPLICANT:  Roman, Mark
;  TITLE OF INVENTION: Immunostimulatory
;  TITLE OF INVENTION:  Polynucleotide/Immunomodulatory Molecule Conjugates
;  FILE REFERENCE: 6510-172CIP
;  CURRENT APPLICATION NUMBER: US/09/308,036A
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: PCT/US97/19004
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: 60/028,118
;  PRIOR FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DY1018 polynucleotide
US-09-308-036A-1

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 18
US-09-791-500-1
; Sequence 1, Application US/09791500
; Patent No. 6613751
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Rachmilewitz, Daniel
;  TITLE OF INVENTION: Method for Treating Inflammatory Bowel
;  TITLE OF INVENTION:  Disease and Other Forms of Gastrointestinal Inflammation.
;  FILE REFERENCE: 6510-202US1
;  CURRENT APPLICATION NUMBER: US/09/791,500
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-1

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 19
US-09-107-532A-1566
; Sequence 1566, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 1566:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 813 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...813
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1566:
US-09-107-532A-1566

  Query Match             70.5%;  Score 14.8;  DB 4;  Length 813;
  Best Local Similarity   88.9%;  Pred. No. 66;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              | |||||||||||||| ||
Db        239 TTGTCGAACGTTCGAAAT 256


RESULT 20
US-09-374-174B-1
; Sequence 1, Application US/09374174B
; Patent No. 6554985
; GENERAL INFORMATION:
;  APPLICANT:  Ruiz-Martinez, Maria C.
;  APPLICANT:  Berka, Jan
;  APPLICANT:  Simpson, John W.
;  TITLE OF INVENTION:  Methods and Formulations for the Separation of
;  TITLE OF INVENTION:  Biological Macromolecules
;  FILE REFERENCE:  Cura-31: MegaBACE (15966-531)
;  CURRENT APPLICATION NUMBER: US/09/374,174B
;  CURRENT FILING DATE:  1999-08-13
;  PRIOR APPLICATION NUMBER:  USSN 60/107,798
;  PRIOR FILING DATE:  1998-11-10
;  NUMBER OF SEQ ID NOS:  5
```

```
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1069
;   TYPE: DNA
;   ORGANISM: Bacteriophage M13mp18
;   FEATURE:
;   OTHER INFORMATION: Wherein an "N" between residues 811 to 1069 may be
;   OTHER INFORMATION: G, A, T or C
US-09-374-174B-1

  Query Match             70.5%;  Score 14.8;  DB 4;  Length 1069;
  Best Local Similarity   88.9%;  Pred. No. 68;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATG 19
              |||||||||| ||||| |
Db        671 CGTCGAACGTGCGAGAAG 688


RESULT 21
US-09-252-991A-2256
; Sequence 2256, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 2256
;   LENGTH: 1497
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2256

  Query Match             70.5%;  Score 14.8;  DB 4;  Length 1497;
  Best Local Similarity   88.9%;  Pred. No. 71;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              ||| |||||| |||||||
Db       1218 TCGGCGAACGATCGAGAT 1235


RESULT 22
US-09-252-991A-2425/c
; Sequence 2425, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 2425
;   LENGTH: 1950
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2425

  Query Match             70.5%;  Score 14.8;  DB 4;  Length 1950;
  Best Local Similarity   88.9%;  Pred. No. 74;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              ||| |||||| |||||||
Db        847 TCGGCGAACGATCGAGAT 830


RESULT 23
US-08-446-794A-5
; Sequence 5, Application US/08446794A
; Patent No. 5747327
;  GENERAL INFORMATION:
;    APPLICANT:  UEKI, JUN
;    APPLICANT:  MORIOKA, SHINJI
;    TITLE OF INVENTION:  PHOSPHOLIPASE D GENE ORIGINATED FROM
;    TITLE OF INVENTION:  PLANT
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH AND BIRCH
;      STREET:  P.O. BOX 747
;      CITY:  FALLS CHURCH
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,794A
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURPHY JR, GERALD M
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  0760-0203P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-205-8000
;      TELEFAX:  703-205-8050
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2799 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1876..1983
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2524..2799
US-08-446-794A-5

  Query Match             70.5%;  Score 14.8;  DB 1;  Length 2799;
  Best Local Similarity   88.9%;  Pred. No. 77;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              ||| ||||||||| ||||
Db        751 GTCAAACGTTCGATATGA 768


RESULT 24
US-08-750-007-4
; Sequence 4, Application US/08750007
; Patent No. 5801016
;  GENERAL INFORMATION:
;    APPLICANT:  MORIOKA, SHINJI
;    APPLICANT:  UEKI, JUN
;    TITLE OF INVENTION:  DNA FRAGMENT, RECOMBINANT VECTOR
```

```
;    TITLE OF INVENTION:  CONTAINING THE SAME AND METHOD FOR EXPRESSING FOREIGN
;    TITLE OF INVENTION:  GENES USING THE SAME
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH AND BIRCH
;      STREET:  PO BOX 747
;      CITY:  FALLS CHURCH
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/750,007
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURPHY JR, GERALD M
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  0760-221P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2799 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1876..1983
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2524..2799
US-08-750-007-4

  Query Match             70.5%;  Score 14.8;  DB 1;  Length 2799;
  Best Local Similarity   88.9%;  Pred. No. 77;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              ||| |||||||||| ||||
Db        751 GTCAAACGTTCGATATGA 768


RESULT 25
US-09-621-976-12664
; Sequence 12664, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 12664
;   LENGTH: 424
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-12664

  Query Match             69.5%;  Score 14.6;  DB 4;  Length 424;
  Best Local Similarity   81.0%;  Pred. No. 78;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||| || ||| || |||||
Db        115 TCGTCAAAGGTTTGAAATGAT 135


RESULT 26
US-09-221-017B-893
; Sequence 893, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
;    APPLICANT:  Ross, Bruce C.
;    TITLE OF INVENTION:  P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
;    NUMBER OF SEQUENCES:  1120
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:.  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/221,017B
;      FILING DATE:  23-DEC-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP1182
;      FILING DATE:  31-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP1546
;      FILING DATE:  30-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP2911
;      FILING DATE:  09-APR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/AU98/01023
;      FILING DATE:  10-DEC-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monroy, Gladys H
;      REGISTRATION NUMBER:  32,430
;      REFERENCE/DOCKET NUMBER:  27340-20021.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  893:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3468 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  UNKNOWN
;    ORIGINAL SOURCE:
;      ORGANISM:  PORYPHYROMONAS GINGIVALIS
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1...3468
US-09-221-017B-893

  Query Match             69.5%;  Score 14.6;  DB 4;  Length 3468;
  Best Local Similarity   81.0%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||||  | ||||||| ||||
Db       1936 TCGTCGTGCTTTCGAGGTGAT 1956
```

```
RESULT 27
US-08-399-412A-58
; Sequence 58, Application US/08399412A
; Patent No. 5622828
;  GENERAL INFORMATION:
;    APPLICANT:  Parma, David
;    APPLICANT:  Gold, Larry
;    TITLE OF INVENTION:  High-Affinity Oligonucleotide
;    TITLE OF INVENTION:  Ligands To Secretory Phospholipase
;    TITLE OF INVENTION:  A2 (sPLA2)
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MB storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/399,412A
;      FILING DATE:  6-MARCH-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Julie L. Bernard
;      REGISTRATION NUMBER:  36,450
;      REFERENCE/DOCKET NUMBER:  NEX27
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  77 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-399-412A-58

  Query Match             68.6%;  Score 14.4;  DB 1;  Length 77;
  Best Local Similarity   75.0%;  Pred. No. 80;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CGAACGTTCGAGATGA 20
              ||||||::||| |:||
Db         48 CGAACGUUCGACAUGA 63


RESULT 28
US-08-447-169A-36
; Sequence 36, Application US/08447169A
; Patent No. 5811533
;  GENERAL INFORMATION:
;    APPLICANT:  JANJIC, N. and GOLD, L.
;    TITLE OF INVENTION:  HIGH-AFFINITY OLIGONUCLEOTIDE
;    TITLE OF INVENTION:  LIGANDS TO VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR (VEGF)
;    NUMBER OF SEQUENCES:  242
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Place, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MG storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,169A
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/233,012
;      FILING DATE:  25-APRIL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/205,515
;      FILING DATE:  03-MARCH-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  77 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-447-169A-36

  Query Match             67.6%;  Score 14.2;  DB 1;  Length 77;
  Best Local Similarity   63.2%;  Pred. No. 1e+02;
  Matches   12;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGA 20
              ||: || ||::||| |:||
Db         45 CGUAGAGCGUUCGACAUGA 63


RESULT 29
US-08-233-012C-36
; Sequence 36, Application US/08233012C
; Patent No. 5849479
;  GENERAL INFORMATION:
;    APPLICANT:  JANJIC, N. and GOLD, L.
;    TITLE OF INVENTION:  HIGH-AFFINITY OLIGONUCLEOTIDE
;    TITLE OF INVENTION:  LIGANDS TO VASCULAR
;    TITLE OF INVENTION:  ENDOTHELIAL GROWTH FACTOR
;    TITLE OF INVENTION:
;    NUMBER OF SEQUENCES:  146
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Place, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
```

```
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MG
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/233,012C
;      FILING DATE:  25-APRIL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  77 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-233-012C-36

  Query Match             67.6%;  Score 14.2;  DB 2;  Length 77;
  Best Local Similarity   63.2%;  Pred. No. 1e+02;
  Matches   12;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGA 20
              ||: || ||::||| |:||
Db         45 CGUAGAGCGUUCGACAUGA 63


RESULT 30
US-09-848-295-1
; Sequence 1, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
;  TITLE OF INVENTION:  Thereon
;  FILE REFERENCE: PF527
;  CURRENT APPLICATION NUMBER: US/09/848,295
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: 60/202,193
;  PRIOR FILING DATE: 2000-05-05
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1535
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(579)
US-09-848-295-1

  Query Match             67.6%;  Score 14.2;  DB 4;  Length 1535;
  Best Local Similarity   84.2%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGAT 21
              |||||| ||||||||  ||
Db       1467 GTCGAAAGTTCGAGACCAT 1485


RESULT 31
US-08-956-171E-203
; Sequence 203, Application US/08956171E
; Patent No. 6593114
;   GENERAL INFORMATION:
;        APPLICANT: Charles Kunsch
;                   Gil H. Choi
;                   Patrick S. Dillon
;                   Craig A. Rosen
;                   Steven C. Barash
;                   Michael R. Fannon
;        TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;        NUMBER OF SEQUENCES: 5256
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/956,171E
;             FILING DATE: 20-Oct-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/009,861
;             FILING DATE: January 5, 1996
;             APPLICATION NUMBER: 08/781,986
;             FILING DATE: January 3, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mark J. Hyman
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB248P1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (240) 314-1224
;             TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 203:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 4715 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 203:
US-08-956-171E-203

  Query Match             67.6%;  Score 14.2;  DB 4;  Length 4715;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGA 20
              |||  || ||||||||||
Db       1285 CGTTAAAAGTTCGAGATGA 1303


RESULT 32
US-09-173-914-6/c
; Sequence 6, Application US/09173914
; Patent No. 6171857
; GENERAL INFORMATION:
;  APPLICANT: Hendrickson, Eric
;  TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and
;  TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity
;  FILE REFERENCE: B0877/7017/HK
;  CURRENT APPLICATION NUMBER: US/09/173,914
```

```
;  CURRENT FILING DATE: 1998-10-16
;  EARLIER APPLICATION NUMBER: 60/064,557
;  EARLIER FILING DATE: 1997-10-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 14636
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-173-914-6

  Query Match             67.6%;  Score 14.2;  DB 3;  Length 14636;
  Best Local Similarity   84.2%;  Pred. No. 2e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGA 20
              | || |||||| |||||||
Db       1050 CTTCAAACGTTTGAGATGA 1032


RESULT 33
US-09-428-517-1/c
; Sequence 1, Application US/09428517
; Patent No. 6251636
; GENERAL INFORMATION:
;  APPLICANT: Betlach, Mary C.
;  APPLICANT: Shah, Sanjay Krishnakant
;  APPLICANT: McDaniel, Robert
;  APPLICANT: Tang, Li
;  TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
;  FILE REFERENCE: 30062-20029.00
;  CURRENT APPLICATION NUMBER: US/09/428,517
;  CURRENT FILING DATE: 1999-10-28
;  EARLIER APPLICATION NUMBER: 60/120,254
;  EARLIER FILING DATE: 1999-02-16
;  EARLIER APPLICATION NUMBER: 60/106,100
;  EARLIER FILING DATE: 1998-10-29
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 50937
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artifical Sequence: Recombinant DNA
US-09-428-517-1

  Query Match             67.6%;  Score 14.2;  DB 3;  Length 50937;
  Best Local Similarity   84.2%;  Pred. No. 2.4e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              ||||||||||| || | ||
Db       5439 TCGTCGAACGTCCGGGCTG 5421


RESULT 34
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             67.6%;  Score 14.2;  DB 3;  Length 4403765;
  Best Local Similarity   84.2%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGAT 21
              ||||  |||||||||||| |
Db    1399888 GTCGCCCGTTCGAGATGGT 1399870


RESULT 35
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             67.6%;  Score 14.2;  DB 3;  Length 4411529;
  Best Local Similarity   84.2%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGAT 21
              ||||  |||||||||||| |
Db    1400419 GTCGCCCGTTCGAGATGGT 1400401


RESULT 36
US-09-296-477-15
; Sequence 15, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
;   LENGTH: 22
```

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (11)...(11)
;   OTHER INFORMATION: 5-bromocytosine
US-09-296-477-15

  Query Match             66.7%;  Score 14;  DB 4;  Length 22;
  Best Local Similarity   93.3%;  Pred. No. 1.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              ||| ||||||||||||
Db          8 GAANGTTCGAGATGA 22


RESULT 37
US-08-710-134-63/c
; Sequence 63, Application US/08710134
; Patent No. 5834181
;  GENERAL INFORMATION:
;    APPLICANT:  SHUBER, ANTHONY P.
;    TITLE OF INVENTION:  HIGH THROUGHPUT SCREENING METHOD FOR
;    TITLE OF INVENTION:  SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genzyme Corporation
;      STREET:  One Mountain Road
;      CITY:  Framingham
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  01701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/710,134
;      FILING DATE:  13-SEP-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dugan, Deborah A.
;      REGISTRATION NUMBER:  37,315
;      REFERENCE/DOCKET NUMBER:  IGS-8.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  508-872-8400
;      TELEFAX:  508-872-5415
;  INFORMATION FOR SEQ ID NO:  63:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  66 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Oligonucleotides"
US-08-710-134-63

  Query Match             65.7%;  Score 13.8;  DB 2;  Length 66;
  Best Local Similarity   88.2%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATGA 20
              |||| || |||||||||
Db         51 TCGATCGATCGAGATGA 35


RESULT 38
US-08-485-885-63/c
; Sequence 63, Application US/08485885
; Patent No. 5849483
;  GENERAL INFORMATION:
;    APPLICANT:  SHUBER, ANTHONY P.
;    TITLE OF INVENTION:  HIGH THROUGHPUT SCREENING METHOD FOR
;    TITLE OF INVENTION:  SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genzyme Corporation
;      STREET:  One Mountain Road
;      CITY:  Framingham
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  01701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,885
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dugan, Deborah A.
;      REGISTRATION NUMBER:  37,315
;      REFERENCE/DOCKET NUMBER:  GEN4-12.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  508-872-8400
;      TELEFAX:  508-872-5415
;  INFORMATION FOR SEQ ID NO:  63:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  66 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Oligonucleotides"
US-08-485-885-63

  Query Match             65.7%;  Score 13.8;  DB 2;  Length 66;
  Best Local Similarity   88.2%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATGA 20
              |||| || |||||||||
Db         51 TCGATCGATCGAGATGA 35


RESULT 39
US-08-710-134-64/c
; Sequence 64, Application US/08710134
; Patent No. 5834181
;  GENERAL INFORMATION:
;    APPLICANT:  SHUBER, ANTHONY P.
;    TITLE OF INVENTION:  HIGH THROUGHPUT SCREENING METHOD FOR
;    TITLE OF INVENTION:  SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genzyme Corporation
;      STREET:  One Mountain Road
;      CITY:  Framingham
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  01701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/710,134
;      FILING DATE:  13-SEP-1996
;      CLASSIFICATION:  435
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dugan, Deborah A.
;      REGISTRATION NUMBER:  37,315
;      REFERENCE/DOCKET NUMBER:  IG5-8.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  508-872-8400
;      TELEFAX:  508-872-5415
;  INFORMATION FOR SEQ ID NO:  64:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  86 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Oligonucleotides"
US-08-710-134-64

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  Best Local Similarity   88.2%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATGA 20
              |||| || |||||||||
Db         70 TCGATCGATCGAGATGA 54


RESULT 40
US-08-485-885-64/c
; Sequence 64, Application US/08485885
; Patent No. 5849483
;  GENERAL INFORMATION:
;    APPLICANT:  SHUBER, ANTHONY P.
;    TITLE OF INVENTION:  HIGH THROUGHPUT SCREENING METHOD FOR
;    TITLE OF INVENTION:  SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genzyme Corporation
;      STREET:  One Mountain Road
;      CITY:  Framingham
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  01701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,885
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dugan, Deborah A.
;      REGISTRATION NUMBER:  37,315
;      REFERENCE/DOCKET NUMBER:  GEN4-12.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  508-872-8400
;      TELEFAX:  508-872-5415
;  INFORMATION FOR SEQ ID NO:  64:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  86 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Oligonucleotides"
US-08-485-885-64

  Query Match             65.7%;  Score 13.8;  DB 2;  Length 86;
  Best Local Similarity   88.2%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATGA 20
              |||| || |||||||||
Db         70 TCGATCGATCGAGATGA 54


Search completed: April  6, 2004, 03:58:41
Job time : 114 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 6, 2004, 01:36:06 ; Search time 3183 Seconds
(without alignments)
197.017 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgtcgaacgttcgagatgat 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID		Description
	1	18.4	87.6	802	29	CNS04SNV	AL305428	Tetraodon
	2	17.8	84.8	302	14	CD182992	CD182992	MS1-0037T
c	3	17.8	84.8	441	14	CD156376	CD156376	ML1-0046T
	4	17.8	84.8	586	14	CD124255	CD124255	ME1-0086G
c	5	17.8	84.8	785	14	CF434519	CF434519	EST670864
	6	16.8	80.0	221	14	CD572389	CD572389	PBL_20_H0
c	7	16.8	80.0	461	14	CA707068	CA707068	wdk2c.pk0
	8	16.8	80.0	587	14	CA827269	CA827269	1114012C1
c	9	16.8	80.0	595	28	BH387860	BH387860	AG-ND-129
	10	16.8	80.0	1410	10	BE052250	BE052250	GA__Ea003
c	11	16.4	78.1	303	10	AW710594	AW710594	e4h01ne.r
	12	16.4	78.1	424	13	BW170465	BW170465	BW170465
	13	16.4	78.1	439	12	BI515898	BI515898	BB160020B
c	14	16.4	78.1	445	13	BW300285	BW300285	BW300285
c	15	16.4	78.1	457	12	BP018564	BP018564	BP018564
c	16	16.4	78.1	504	28	B29433	B29433	F19L12TFB I
	17	16.4	78.1	511	12	BI514876	BI514876	BB160016B
	18	16.4	78.1	511	12	BI514893	BI514893	BB160016B
	19	16.4	78.1	635	13	BW118728	BW118728	BW118728
	20	16.4	78.1	650	9	AV902415	AV902415	AV902415
	21	16.4	78.1	662	13	BW174317	BW174317	BW174317
	22	16.4	78.1	663	13	BW171245	BW171245	BW171245
c	23	16.4	78.1	707	13	BW297679	BW297679	BW297679
c	24	16.4	78.1	709	13	BW303599	BW303599	BW303599
	25	16.4	78.1	726	13	BW174467	BW174467	BW174467
	26	16.4	78.1	914	29	CNS04AO0	AL282105	Tetraodon
	27	16.2	77.1	166	14	CA196886	CA196886	SCBFAD109
c	28	16.2	77.1	273	12	BG931701	BG931701	h112-118
c	29	16.2	77.1	314	14	CD190559	CD190559	MS1-0064U
	30	16.2	77.1	315	14	CD183371	CD183371	MS1-0038U
	31	16.2	77.1	328	12	BI075646	BI075646	IP1_23_C0
c	32	16.2	77.1	329	14	CD177754	CD177754	MS1-0011T
c	33	16.2	77.1	342	14	CD092357	CD092357	MC1-0096T
	34	16.2	77.1	374	28	AQ840347	AQ840347	nbxb0055D
c	35	16.2	77.1	375	14	CD190376	CD190376	MS1-0064U
c	36	16.2	77.1	377	14	CD178552	CD178552	MS1-0014P
c	37	16.2	77.1	384	14	CD187006	CD187006	MS1-0056U
c	38	16.2	77.1	384	14	CD190545	CD190545	MS1-0064U
c	39	16.2	77.1	392	14	CD124011	CD124011	ME1-0084T
c	40	16.2	77.1	410	10	AW699669	AW699669	gb30d06.y
c	41	16.2	77.1	412	10	AW497269	AW497269	ga57c10.y
c	42	16.2	77.1	414	14	CD096098	CD096098	ME1-0006T
c	43	16.2	77.1	428	12	BJ195526	BJ195526	BJ195526
	44	16.2	77.1	428	14	CF431104	CF431104	NIT1_6_D1
	45	16.2	77.1	434	14	CF431883	CF431883	NIT1_11_E

ALIGNMENTS

RESULT 1
CNS04SNV
LOCUS CNS04SNV 802 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 007J10 of library H from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL305428
VERSION AL305428.1 GI:8197678
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645
REFERENCE 2
AUTHORS Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,

```
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 802)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
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     source          1. .802
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="007J10"
                     /clone_lib="H"
                     /note="Genoscope sequence ID : C0BH007DE05XD1~end : T7"
ORIGIN

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  Best Local Similarity   95.0%;  Pred. No. 2.6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              ||||||||||| |||||||||
Db        623 CGTCGAACGTGCGAGATGAT 642


RESULT 2
CD182992
LOCUS       CD182992                302 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  MS1-0037T-D120-A09-U.G MS1-0037 Schistosoma mansoni cDNA clone
            MS1-0037T-D120-A09.G, mRNA sequence.
ACCESSION   CD182992
VERSION     CD182992.1  GI:34713214
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 302)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: MS1-0037T-D120  row: 9  column: A.
FEATURES             Location/Qualifiers
     source          1. .302
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                     /mol_type="mRNA"
                     /db_xref="taxon:6183"
                     /clone="MS1-0037T-D120-A09.G"
                     /sex="mixed pool"
                     /dev_stage="schistosomulum"
                     /lab_host="in vitro culture"
                     /clone_lib="MS1-0037"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             84.8%;  Score 17.8;  DB 14;  Length 302;
  Best Local Similarity   90.5%;  Pred. No. 3.8e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||||||||| | ||||||
Db         19 TCGTCGAACGTTTGTGATGAT 39


RESULT 3
CD156376/c
LOCUS       CD156376                441 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  ML1-0046T-M209-C11-U.G ML1-0046 Schistosoma mansoni cDNA clone
            ML1-0046T-M209-C11.G, mRNA sequence.
ACCESSION   CD156376
VERSION     CD156376.1  GI:34693161
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 441)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
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                     /mol_type="mRNA"
                     /db_xref="taxon:6183"
                     /clone="ML1-0046T-M209-C11.G"
                     /sex="mixed pool"
                     /dev_stage="miracidium"
                     /clone_lib="ML1-0046"
                     /note="Vector: pGEM T-easy"
ORIGIN
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  Query Match             84.8%;  Score 17.8;  DB 14;  Length 441;
  Best Local Similarity   90.5%;  Pred. No. 4.3e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||||||||||  | ||||||
Db        376 TCGTCGAACGTTTGTGATGAT 356


RESULT 4
CD124255
LOCUS       CD124255                586 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  ME1-0086G-A185-H02-U.B ME1-0086 Schistosoma mansoni cDNA clone
            ME1-0086G-A185-H02.B, mRNA sequence.
ACCESSION   CD124255
VERSION     CD124255.1  GI:34662288
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 586)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: ME1-0086G-A185  row: 2  column: H.
FEATURES             Location/Qualifiers
     source          1. .586
                     /organism="Schistosoma mansoni"
                     /mol_type="mRNA"
                     /db_xref="taxon:6183"
                     /clone="ME1-0086G-A185-H02.B"
                     /sex="mixed pool"
                     /dev_stage="egg"
                     /lab_host="Mus musculus"
                     /clone_lib="ME1-0086"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             84.8%;  Score 17.8;  DB 14;  Length 586;
  Best Local Similarity   90.5%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||||||||||  | ||||||
Db        373 TCGTCGAACGTTTGTGATGAT 393


RESULT 5
CF434519/c
LOCUS       CF434519                785 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  EST670864 normalized cDNA library of onion Allium cepa cDNA clone
            ACAAA82, mRNA sequence.
ACCESSION   CF434519
VERSION     CF434519.1  GI:34457209
KEYWORDS    EST.
SOURCE      Allium cepa (onion)
  ORGANISM  Allium cepa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
            Allium.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   Havey,M.J., Cheung,F., Van Aken,S., Utterback,T. and Town,C.D.
  TITLE     Expressed Sequence Tags from a normalized library of mixed onion
            tissues (Allium cepa)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Havey MJ
            Department of Horticulture
            USDA-ARS and University of Wisconsin
            1575 Linden Drive, Madison, WI 53706, USA
            Tel: 608-262-1830
            Fax: 608-262-4743
            Email: mjhavey@facstaff.wisc.edu
            TIGR sequence name ACAAA82TR. For more information:
            http://haveylab.hort.wisc.edu
            Seq primer: CAG GAA ACA GCT ATG ACC.
FEATURES             Location/Qualifiers
     source          1. .785
                     /organism="Allium cepa"
                     /mol_type="mRNA"
                     /cultivar="Red Creole(bulbs), unknown(callus), Ebano &
                     Texas Legend(roots)"
                     /db_xref="taxon:4679"
                     /clone="ACAAA82"
                     /tissue_type="Callus, roots, and young bulbs"
                     /clone_lib="normalized cDNA library of onion"
                     /note="Vector: pCMVSport6.1-ccdb (Invitrogen); Site_1:
                     EcoRV (5'); Site_2: NotI (3'); Equal molar amounts of mRNA
                     from callus, roots, and young bulbs were combined to
                     synthesize the library. Normalization to enrich for
                     low-copy transcripts was performed by proprietary
                     techniques of Invitrogen."
ORIGIN

  Query Match             84.8%;  Score 17.8;  DB 14;  Length 785;
  Best Local Similarity   90.5%;  Pred. No. 5.1e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              | |||||  ||||||||||||
Db         65 TTGTCGATCGTTCGAGATGAT 45


RESULT 6
CD572389
LOCUS       CD572389                221 bp    mRNA    linear   EST 12-JUN-2003
DEFINITION  PBL_20_H02 Porcine Brain Library Sus scrofa cDNA clone PBL 5', mRNA
            sequence.
ACCESSION   CD572389
VERSION     CD572389.1  GI:31663456
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 221)
  AUTHORS   Nobis,W., Ren,X., Suchyta,S.P., Zanell,A.J. and Coussens,P.M.
  TITLE     Development of a porcine brain cDNA library, EST database and
            microarray resource
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Paul Coussens
            Michigan State University
            1205H Anthony Hall, East Lansing, MI 48824, USA
```

```
            Email: coussens@msu.edu
            Seq primer: M13.
FEATURES              Location/Qualifiers
     source           1. .221
                      /organism="Sus scrofa"
                      /mol_type="mRNA"
                      /db_xref="taxon:9823"
                      /clone="PBL"
                      /sex="male and female"
                      /tissue_type="Brain and central nervous system"
                      /dev_stage="fetal, 10-day, 21-day, 5-week, mature boar,
                      post-pubertal gilt, lactating sow"
                      /clone_lib="Porcine Brain Library"
                      /note="Porcine (Pig) brain library includes pre-frontal
                      cortex, frontal  cortex, hippocampus, hypothalamus,
                      parietal cortex, amygdala,  cerebellum, spinal cord, eye,
                      accumbens, and fetal pig CNS"
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 14;  Length 221;
  Best Local Similarity   90.0%;  Pred. No. 1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              |||||||| || ||||||||
Db         33 CGTCGAACTTTTGAGATGAT 52


RESULT 7
CA707068/c
LOCUS       CA707068                461 bp    mRNA    linear   EST 26-NOV-2002
DEFINITION  wdk2c.pk0004.g12 wdk2c Triticum aestivum cDNA clone
            wdk2c.pk0004.g12 5' end, mRNA sequence.
ACCESSION   CA707068
VERSION     CA707068.1  GI:25428861
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 461)
  AUTHORS   Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
            Miao,G., Caraher,N. and Hanafey,M.K.
  TITLE     DuPont Wheat cDNA Sequence
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Scott V. Tingey
            Crop Genetics
            E. I. DuPont de Nemours and Company
            1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
            Tel: 302-631-2602
            Fax: 302-631-2607
            Email: Scott.V.Tingey@USA.dupont.com
            Seq primer: M13.
FEATURES              Location/Qualifiers
     source           1. .461
                      /organism="Triticum aestivum"
                      /mol_type="mRNA"
                      /db_xref="taxon:4565"
                      /clone="wdk2c.pk0004.g12"
                      /tissue_type="kernel"
                      /clone_lib="wdk2c"
                      /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
                      XhoI; Wheat (Triticum aestivum L.) developing kernel, 7
                      days after anthesis."
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 14;  Length 461;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGATGAT 21
              || |||||||| ||||||||
Db        293 CGGCGAACGTTGGAGATGAT 274


RESULT 8
CA827269
LOCUS       CA827269                587 bp    mRNA    linear   EST 11-DEC-2002
DEFINITION  1114012C10.y1 1114 - Unigene IV from Maize Genome Project Zea mays
            cDNA, mRNA sequence.
ACCESSION   CA827269
VERSION     CA827269.1  GI:26455686
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 587)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1114012  row: C  column: 10.
FEATURES              Location/Qualifiers
     source           1. .587
                      /organism="Zea mays"
                      /mol_type="mRNA"
                      /db_xref="dbEST:3524_1_56_1_G06.y_1"
                      /db_xref="taxon:4577"
                      /clone_lib="1114 - Unigene IV from Maize Genome Project"
                      /note="This library represents the unique genes found in
                      the fourth round of EST sequencing at Stanford University
                      for the maize genome project. Sequences are present from
                      libraries 1091 and 3524. Contigs were assembled using
                      ZmDBAssembler and 2 representatives from each contig were
                      selected for the Unigene set. All singlets were also
                      selected."
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 14;  Length 587;
  Best Local Similarity   90.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGA 20
              ||||| | ||||||||||||
Db         30 TCGTCCAGCGTTCGAGATGA 49


RESULT 9
BH387860/c
LOCUS       BH387860                595 bp    DNA     linear   GSS 11-DEC-2001
DEFINITION  AG-ND-129F22.TF ND-TAM Anopheles gambiae genomic clone
            AG-ND-129F22, genomic survey sequence.
ACCESSION   BH387860
VERSION     BH387860.1  GI:17334001
KEYWORDS    GSS.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Anopheles.
REFERENCE   1  (bases 1 to 595)
  AUTHORS   Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J.,
            Ren,C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B.,
            Gardner,M.J. and Collins,F.H.
  TITLE     Construction of a BAC library and generation of BAC end
            sequence-tagged connectors for genome sequencing of the African
```

malaria mosquito Anopheles gambiae
JOURNAL Mol. Genet. Genomics 268 (6), 720-728 (2003)
MEDLINE 22542063
PUBMED 12655398
COMMENT Other_GSSs: AG-ND-129F22.TR
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
Seq primer: M13 For
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .595
/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-129F22"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
ORIGIN

Query Match 80.0%; Score 16.8; DB 28; Length 595;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGA 20
|||| ||||||| |||||||
Db 177 TCGTGGAACGTTGGAGATGA 158

RESULT 10
BE052250
LOCUS BE052250 1410 bp mRNA linear EST 08-MAR-2001
DEFINITION GA__Ea0035L13f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA__Ea0035L13f, mRNA sequence.
ACCESSION BE052250
VERSION BE052250.1 GI:8379306
KEYWORDS EST.
SOURCE Gossypium arboreum
ORGANISM Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE 1 (bases 1 to 1410)
AUTHORS Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
TITLE An integrated analysis of the genetics, development, and evolution of the cotton fiber
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence start: 13
High quality sequence stop: 501.
FEATURES Location/Qualifiers
source 1. .1410
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA__Ea0035L13f"
/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
ORIGIN

Query Match 80.0%; Score 16.8; DB 10; Length 1410;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGA 20
|||||||||| ||||||||
Db 1356 TCGTCGAACGAGCGAGATGA 1375

RESULT 11
AW710594/c
LOCUS AW710594 303 bp mRNA linear EST 25-APR-2000
DEFINITION e4h01ne.r1 Neurospora crassa evening cDNA library Neurospora crassa cDNA clone e4h01ne 3', mRNA sequence.
ACCESSION AW710594
VERSION AW710594.1 GI:7599686
KEYWORDS EST.
SOURCE Neurospora crassa
ORGANISM Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE 1 (bases 1 to 303)
AUTHORS Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
TITLE Two Neurospora crassa EST Databases
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: e4h01ne.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Seq primer: Universal Reverse Primer
High quality sequence stop: 255.
FEATURES Location/Qualifiers
source 1. .303
/organism="Neurospora crassa"
/mol_type="mRNA"
/strain="Strain 30-7 (bd; A)"
/db_xref="taxon:5141"
/clone="e4h01ne"
/tissue_type="tissue harvested following 22hr growth in dark"
/clone_lib="Neurospora crassa evening cDNA library"
/note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2: EcoRI; See: Bell-Perdersen,D., et al. PNAS 93:13096,1996. 5' end of cDNA cloned into XbaI site of pBluescript; 3' end of cDNA cloned into EcoRI site of pBluescript"
ORIGIN

Query Match 78.1%; Score 16.4; DB 10; Length 303;
Best Local Similarity 94.4%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCGAACGTTCGAGATGA 20
|||||||||| ||||||
Db 232 GTCGAACGTTCAAGATGA 215

```
RESULT 12
BW170465
LOCUS       BW170465                424 bp    mRNA    linear   EST 04-NOV-2002
DEFINITION  BW170465 Nori Satoh unpublished cDNA library, neural complex Ciona
            intestinalis cDNA clone rcinc008n07 3', mRNA sequence.
ACCESSION   BW170465
VERSION     BW170465.1  GI:24560352
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 424)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .424
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcinc008n07"
                     /tissue_type="neural complex"
                     /clone_lib="Nori Satoh unpublished cDNA library, neural
                     complex"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 13;  Length 424;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              ||||||||| ||||||||
Db        340 TCGTCGAACATTCGAGAT 357


RESULT 13
BI515898
LOCUS       BI515898                439 bp    mRNA    linear   EST 08-APR-2002
DEFINITION  BB160020B20D02.5 Bee Brain Normalized Library, BB16 Apis mellifera
            cDNA clone BB160020B20D02 5', mRNA sequence.
ACCESSION   BI515898
VERSION     BI515898.1  GI:15366272
KEYWORDS    EST.
SOURCE      Apis mellifera (honeybee)
  ORGANISM  Apis mellifera
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
            Apidae; Apis.
REFERENCE   1  (bases 1 to 439)
  AUTHORS   Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L.,
            Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
  TITLE     Annotated expressed sequence tags and cDNA microarrays for studies
            of brain and behavior in the honey bee
  JOURNAL   Genome Res. 12 (4), 555-566 (2002)
  MEDLINE   21929762
   PUBMED   11932240
COMMENT     Contact: Gene E. Robinson
            Department of Entomology
            University of Illinois
            505 S. Goodwin Ave., Urbana, IL 61801, USA
            Tel: 217 265 0309
            Fax: 217 244 3499
            Email: generobi@life.uiuc.edu
            This research was funded by the University of Illinois Critical
            Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
            Award in Functional Genomics to G.E. Robinson and an NSF
            Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
            PCR PRimers
            FORWARD: TAATACGACTCACTATAGGG
            BACKWARD: ATTAACCCTCACTAAAG
            Plate: BB160020B20  row: D  column: 02
            Seq primer: AGCGGATAACAATTTCACACAGGA
            High quality sequence stop: 439.
FEATURES             Location/Qualifiers
     source          1. .439
                     /organism="Apis mellifera"
                     /mol_type="mRNA"
                     /strain="mixed strains of European bees, predominantly
                     A.m. ligustica"
                     /db_xref="taxon:7460"
                     /clone="BB160020B20D02"
                     /sex="female"
                     /tissue_type="brain"
                     /dev_stage="adult worker honey bee"
                     /lab_host="DH10B"
                     /clone_lib="Bee Brain Normalized Library, BB16"
                     /note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1;
                     Site_2: Not1; The BB16 library was contributed by the
                     Soares laboratory and it was  constructed and normalized
                     as described by Bonaldo, M.F., Lennon, G.  and Soares,
                     M.B. (1996), Genome Research 6(9): 791-806. RNA was
                     prepared from dissected brains of adult worker bees of
                     various ages  and various behavioral groups. "
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 12;  Length 439;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATGAT 21
              |||||||||||||| ||||
Db        269 TCGAACGTTCGAGTTGAT 286


RESULT 14
BW300285/c
LOCUS       BW300285                445 bp    mRNA    linear   EST 11-NOV-2002
DEFINITION  BW300285 Nori Satoh unpublished cDNA library, neural complex Ciona
            intestinalis cDNA clone cinc008n07 5', mRNA sequence.
ACCESSION   BW300285
VERSION     BW300285.1  GI:24880896
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 445)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .445
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cinc008n07"
                     /tissue_type="neural complex"
                     /clone_lib="Nori Satoh unpublished cDNA library, neural
                     complex"
ORIGIN
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  Query Match             78.1%;  Score 16.4;  DB 13;  Length 445;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              |||||||||  ||||||||
Db         80 TCGTCGAACATTCGAGAT 63


RESULT 15
BP018564/c
LOCUS       BP018564                457 bp    mRNA    linear   EST 15-MAR-2002
DEFINITION  BP018564 Nori Satoh unpublished cDNA library, young adult Ciona
            intestinalis cDNA clone ciad54l23 5', mRNA sequence.
ACCESSION   BP018564
VERSION     BP018564.1  GI:19510514
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="ciad54l23"
                     /tissue_type="whole animal"
                     /dev_stage="young adult"
                     /clone_lib="Nori Satoh unpublished cDNA library, young
                     adult"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 12;  Length 457;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              |||||||||  ||||||||
Db        348 TCGTCGAACATTCGAGAT 331


RESULT 16
B29433/c
LOCUS       B29433                  504 bp    DNA     linear   GSS 13-OCT-1997
DEFINITION  F19L12TFB IGF Arabidopsis thaliana genomic clone F19L12, genomic
            survey sequence.
ACCESSION   B29433
VERSION     B29433.1  GI:2515399
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 504)
  AUTHORS   Rounsley,S.D., Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D. and
            Venter,J.C.
  TITLE     Use of a BAC End Sequence Database To Identify Minimal Overlaps for
            Arabidopsis Genomic Sequencing
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: F19L12TR
            Contact: Steve Rounsley
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: rounsley@tigr.org
            Seq primer: M13-21
            Class: BAC ends
            High quality sequence stop: 504.
FEATURES             Location/Qualifiers
     source          1. .504
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia"
                     /db_xref="taxon:3702"
                     /clone="F19L12"
                     /sex="hermaphrodite"
                     /clone_lib="IGF"
                     /note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
                     Produced by Thomas Altmann"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 28;  Length 504;
  Best Local Similarity   94.4%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATGAT 21
              ||||  ||||||||||||||
Db        359 TCGATCGTTCGAGATGAT 342


RESULT 17
BI514876
LOCUS       BI514876                511 bp    mRNA    linear   EST 08-APR-2002
DEFINITION  BB160016B10G01.5 Bee Brain Normalized Library, BB16 Apis mellifera
            cDNA clone BB160016B10G01 5', mRNA sequence.
ACCESSION   BI514876
VERSION     BI514876.1  GI:15365250
KEYWORDS    EST.
SOURCE      Apis mellifera (honeybee)
  ORGANISM  Apis mellifera
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
            Apidae; Apis.
REFERENCE   1  (bases 1 to 511)
  AUTHORS   Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L.,
            Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
  TITLE     Annotated expressed sequence tags and cDNA microarrays for studies
            of brain and behavior in the honey bee
  JOURNAL   Genome Res. 12 (4), 555-566 (2002)
  MEDLINE   21929762
   PUBMED   11932240
COMMENT     Contact: Gene E. Robinson
            Department of Entomology
            University of Illinois
            505 S. Goodwin Ave., Urbana, IL 61801, USA
            Tel: 217 265 0309
            Fax: 217 244 3499
            Email: generobi@life.uiuc.edu
            This research was funded by the University of Illinois Critical
            Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
            Award in Functional Genomics to G.E. Robinson and an NSF
            Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
            PCR PRimers
            FORWARD: TAATACGACTCACTATAGGG
            BACKWARD: ATTAACCCTCACTAAAG
            Plate: BB160016B10  row: G  column: 01
            Seq primer: AGCGGATAACAATTTCACACAGGA
            High quality sequence stop: 511.
FEATURES             Location/Qualifiers
     source          1. .511
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/organism="Apis mellifera"
/mol_type="mRNA"
/strain="mixed strains of European bees, predominantly A.m. ligustica"
/db_xref="taxon:7460"
/clone="BB160016B10G01"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/clone_lib="Bee Brain Normalized Library, BB16"
/note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1; Site_2: Not1; The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups. "

.ORIGIN

Query Match 78.1%; Score 16.4; DB 12; Length 511;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          4 TCGAACGTTCGAGATGAT 21
              |||||||||||||| ||||
Db        401 TCGAACGTTCGAGTTGAT 418
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RESULT 18
BI514893
LOCUS BI514893 511 bp mRNA linear EST 08-APR-2002
DEFINITION BB160016B10H09.5 Bee Brain Normalized Library, BB16 Apis mellifera cDNA clone BB160016B10H09 5', mRNA sequence.
ACCESSION BI514893
VERSION BI514893.1 GI:15365267
KEYWORDS EST.
SOURCE Apis mellifera (honeybee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.
REFERENCE 1 (bases 1 to 511)
AUTHORS Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L., Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
TITLE Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee
JOURNAL Genome Res. 12 (4), 555-566 (2002)
MEDLINE 21929762
PUBMED 11932240
COMMENT Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
Email: generobi@life.uiuc.edu
This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
PCR PRimers
FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
Plate: BB160016B10 row: H column: 09
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 511.
FEATURES Location/Qualifiers
source 1. .511
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="mixed strains of European bees, predominantly A.m. ligustica"
/db_xref="taxon:7460"
/clone="BB160016B10H09"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/clone_lib="Bee Brain Normalized Library, BB16"
/note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1; Site_2: Not1; The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups. "

ORIGIN

Query Match 78.1%; Score 16.4; DB 12; Length 511;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          4 TCGAACGTTCGAGATGAT 21
              |||||||||||||| ||||
Db        401 TCGAACGTTCGAGTTGAT 418
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RESULT 19
BW118728
LOCUS BW118728 635 bp mRNA linear EST 24-OCT-2002
DEFINITION BW118728 Nori Satoh unpublished cDNA library, tailbud embryo Ciona intestinalis cDNA clone rcitb080n02 3', mRNA sequence.
ACCESSION BW118728
VERSION BW118728.1 GI:24365393
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 635)
AUTHORS Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished (2002)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .635
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcitb080n02"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud embryo"

ORIGIN

Query Match 78.1%; Score 16.4; DB 13; Length 635;
Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 TCGTCGAACGTTCGAGAT 18
              |||||||| ||||||||
Db        331 TCGTCGAACATTCGAGAT 348
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RESULT 20
AV902415
LOCUS AV902415 650 bp mRNA linear EST 09-NOV-2001
DEFINITION AV902415 Nori Satoh unpublished cDNA library, young adult Ciona

```
          intestinalis cDNA clone rciad54123 3', mRNA sequence.
ACCESSION   AV902415
VERSION     AV902415.1  GI:16891513
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 650)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .650
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rciad54123"
                     /tissue_type="whole animal"
                     /dev_stage="young adult"
                     /clone_lib="Nori Satoh unpublished cDNA library, young
                     adult"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 9;  Length 650;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              ||||||||| ||||||||
Db        349 TCGTCGAACATTCGAGAT 366


RESULT 21
BW174317
LOCUS       BW174317                662 bp    mRNA    linear   EST 04-NOV-2002
DEFINITION  BW174317 Nori Satoh unpublished cDNA library, neural complex Ciona
            intestinalis cDNA clone rcinc030b19 3', mRNA sequence.
ACCESSION   BW174317
VERSION     BW174317.1  GI:24564241
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 662)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .662
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcinc030b19"
                     /tissue_type="neural complex"
                     /clone_lib="Nori Satoh unpublished cDNA library, neural
                     complex"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 13;  Length 662;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              ||||||||| ||||||||
Db        328 TCGTCGAACATTCGAGAT 345


RESULT 22
BW171245
LOCUS       BW171245                663 bp    mRNA    linear   EST 04-NOV-2002
DEFINITION  BW171245 Nori Satoh unpublished cDNA library, neural complex Ciona
            intestinalis cDNA clone rcinc018d19 3', mRNA sequence.
ACCESSION   BW171245
VERSION     BW171245.1  GI:24561132
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .663
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcinc018d19"
                     /tissue_type="neural complex"
                     /clone_lib="Nori Satoh unpublished cDNA library, neural
                     complex"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 13;  Length 663;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              ||||||||| ||||||||
Db        329 TCGTCGAACATTCGAGAT 346


RESULT 23
BW297679/c
LOCUS       BW297679                707 bp    mRNA    linear   EST 11-NOV-2002
DEFINITION  BW297679 Nori Satoh unpublished cDNA library, neural complex Ciona
            intestinalis cDNA clone cinc018d19 5', mRNA sequence.
ACCESSION   BW297679
VERSION     BW297679.1  GI:24878290
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 707)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
```

```
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .707
                      /organism="Ciona intestinalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:7719"
                      /clone="cinc018d19"
                      /tissue_type="neural complex"
                      /clone_lib="Nori Satoh unpublished cDNA library, neural
                      complex"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 13;  Length 707;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              ||||||||| ||||||||
Db        342 TCGTCGAACATTCGAGAT 325


RESULT 24
BW303599/c
LOCUS       BW303599                709 bp    mRNA    linear   EST 11-NOV-2002
DEFINITION  BW303599 Nori Satoh unpublished cDNA library, neural complex Ciona
            intestinalis cDNA clone cinc030b19 5', mRNA sequence.
ACCESSION   BW303599
VERSION     BW303599.1  GI:24884210
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 709)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .709
                      /organism="Ciona intestinalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:7719"
                      /clone="cinc030b19"
                      /tissue_type="neural complex"
                      /clone_lib="Nori Satoh unpublished cDNA library, neural
                      complex"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 13;  Length 709;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              ||||||||| ||||||||
Db        344 TCGTCGAACATTCGAGAT 327


RESULT 25
BW174467
LOCUS       BW174467                726 bp    mRNA    linear   EST 04-NOV-2002
DEFINITION  BW174467 Nori Satoh unpublished cDNA library, neural complex Ciona
            intestinalis cDNA clone rcinc030j13 3', mRNA sequence.
ACCESSION   BW174467
VERSION     BW174467.1  GI:24564391
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 726)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .726
                      /organism="Ciona intestinalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:7719"
                      /clone="rcinc030j13"
                      /tissue_type="neural complex"
                      /clone_lib="Nori Satoh unpublished cDNA library, neural
                      complex"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 13;  Length 726;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGAT 18
              ||||||||| ||||||||
Db        329 TCGTCGAACATTCGAGAT 346


RESULT 26
CNS04AO0
LOCUS       CNS04AO0                  914 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            095J14 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL282105
VERSION     AL282105.1  GI:8020441
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 914)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
```

```
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="095J14"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG095DE07SP1~end :
                     PUC-Ori"
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 29;  Length 914;
  Best Local Similarity   94.4%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCGAACGTTCGAGATGA 20
              |||||||||||| ||||||
Db        333 GTCGAACGTTCCAGATGA 350


RESULT 27
CA196886
LOCUS       CA196886                 166 bp    mRNA    linear   EST 25-SEP-2003
DEFINITION  SCBFAD1093H09.g AD1 Saccharum officinarum cDNA clone SCBFAD1093H09
            5', mRNA sequence.
ACCESSION   CA196886
VERSION     CA196886.1  GI:35226590
KEYWORDS    EST.
SOURCE      Saccharum officinarum
  ORGANISM  Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE   1  (bases 1 to 166)
  AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
  TITLE     The libraries that made SUCEST
  JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT     Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bcccenter.fcav.unesp.br
            Plate: 093  row: H  column: 09
            Seq primer: T7 Promoter Primer.
FEATURES             Location/Qualifiers
     source          1. .166
                     /organism="Saccharum officinarum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4547"
                     /clone="SCBFAD1093H09"
                     /lab_host="DH10B"
                     /clone_lib="AD1"
                     /note="Organ: seedlings inoculated with Gluconacetobacter
                     diazotroficans; Vector: pSport1; Site_1: SalI; Site_2:
                     NotI; An unidirectional cDNA library generated from
                     [seedlings inoculated with  Gluconacetobacter
                     diazotroficans]. cDNA was prepared from polyA+ mRNA  using
                     SuperScript Plasmid System Kit (Invitrogen). The
                     double-strand  cDNAs were fractionated in a sepharose
                     CL-2B 40cm-columns and fragments  sizing between 0.8 and
                     1.5 Kb were directionally cloned into the vector.  Details
                     of each source of RNA and library construction can be
                     obtained at  http://sucest.lad.ic.unicamp.br/public"
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 14;  Length 166;
  Best Local Similarity   85.7%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||||| ||||||  ||| ||
Db        106 TCGTCGATCGTTCGTGATTAT 126


RESULT 28
BG931701/c
LOCUS       BG931701                 273 bp    mRNA    linear   EST 03-JUL-2002
DEFINITION  h112-118 h112 S. mansoni adult mini-library,
            Fietto/DeMarco/Verjovski-Almeida Schistosoma mansoni cDNA, mRNA
            sequence.
ACCESSION   BG931701
VERSION     BG931701.1  GI:17156638
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 273)
  AUTHORS   Fietto,J.L.R., DeMarco,R. and Verjovski-Almeida,S.
  TITLE     Use of degenerate primers and touchdown PCR for construction of
            cDNA libraries
  JOURNAL   Biotechniques 32 (6), 1404-1408 (2002)
  MEDLINE   22068697
   PUBMED   12074173
COMMENT     Contact: Verjovski-Almeida S
            Departmento de Bioquimica, Instituto de Quimica
            Universidade de Sao Paulo
            Av. Lineu Prestes, 748, Sao Paulo, SP 05508-900, Brasil
            Tel: 55-11-3091-2173
            Fax: 55-11-3091-2186
            Email: verjo@iq.usp.br.
FEATURES             Location/Qualifiers
     source          1. .273
                     /organism="Schistosoma mansoni"
                     /mol_type="mRNA"
                     /strain="BH"
                     /db_xref="taxon:6183"
                     /dev_stage="Adult"
                     /clone_lib="h112 S. mansoni adult mini-library,
                     Fietto/DeMarco/Verjovski-Almeida"
                     /note="Vector: Bluescript SK; minilibrary constructed
                     using low-stringency RT-PCR and consensus-degenerate
                     primer"
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 12;  Length 273;
  Best Local Similarity   85.7%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||| ||| ||||| |||||
Db        250 TCGTCTAACTTTCGACATGAT 230


RESULT 29
CD190559/c
LOCUS       CD190559                 314 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  MS1-0064U-A263-G08-U.B MS1-0064 Schistosoma mansoni cDNA clone
            MS1-0064U-A263-G08.B, mRNA sequence.
ACCESSION   CD190559
VERSION     CD190559.1  GI:34720529
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
```

```
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 314)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: MS1-0064U-A263  row: 8  column: G.
FEATURES             Location/Qualifiers
     source          1. .314
                     /organism="Schistosoma mansoni"
                     /mol_type="mRNA"
                     /db_xref="taxon:6183"
                     /clone="MS1-0064U-A263-G08.B"
                     /sex="mixed pool"
                     /dev_stage="schistosomulum"
                     /lab_host="in vitro culture"
                     /clone_lib="MS1-0064"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 14;  Length 314;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||| ||| ||||| |||||
Db         65 TCGTCTAACTTTCGACATGAT 45


RESULT 30
CD183371
LOCUS       CD183371                315 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  MS1-0038U-A246-C02-U.B MS1-0038 Schistosoma mansoni cDNA clone
            MS1-0038U-A246-C02.B, mRNA sequence.
ACCESSION   CD183371
VERSION     CD183371.1  GI:34713578
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 315)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: MS1-0038U-A246  row: 2  column: C.
FEATURES             Location/Qualifiers
     source          1. .315
                     /organism="Schistosoma mansoni"
                     /mol_type="mRNA"
                     /db_xref="taxon:6183"
                     /clone="MS1-0038U-A246-C02.B"
                     /sex="mixed pool"
                     /dev_stage="schistosomulum"
                     /lab_host="in vitro culture"
                     /clone_lib="MS1-0038"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 14;  Length 315;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||| ||| ||||| |||||
Db        248 TCGTCTAACTTTCGACATGAT 268


RESULT 31
BI075646
LOCUS       BI075646                328 bp    mRNA    linear   EST 20-JUN-2001
DEFINITION  IP1_23_C09.g1_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,
            mRNA sequence.
ACCESSION   BI075646
VERSION     BI075646.1  GI:14514303
KEYWORDS    EST.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 328)
  AUTHORS   Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M. and
            Pratt,L.H.
  TITLE     An EST database from Sorghum: developing preanthesis pannicles
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector and regions
            below Phred quality 16. The threshold for high quality sequence is
            20. Three-prime sequences, which are obtained with PolyTMix or T7
            sequencing primer, are presented as the reverse complement.
            Seq primer: T7
            High quality sequence start: 4
            High quality sequence stop: 328
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .328
```

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                     /organism="Sorghum bicolor"
                     /mol_type="mRNA"
                     /cultivar="BTx623"
                     /db_xref="taxon:4558"
                     /clone_lib="Immature pannicle 1 (IP1)"
                     /note="Organ: Developing preanthesis pannicles; Vector:
                     pBluescript II SK(-) from Lambda Zap II; Site_1: XhoI;
                     Site_2: EcoRI; The library was made from poly-A RNA in the
                     cloning vector lambda ZAP II.  Clones to be sequenced were
                     prepared by mass excision."
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 12;  Length 328;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||||| |||||| ||| ||
Db         25 TCGTCGATCGTTCGTGATTAT 45


RESULT 32
CD177754/c
LOCUS       CD177754                329 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  MS1-0011T-D106-F07-U.G MS1-0011 Schistosoma mansoni cDNA clone
            MS1-0011T-D106-F07.G, mRNA sequence.
ACCESSION   CD177754
VERSION     CD177754.1  GI:34708220
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: MS1-0011T-D106  row: 7  column: F.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Schistosoma mansoni"
                     /mol_type="mRNA"
                     /db_xref="taxon:6183"
                     /clone="MS1-0011T-D106-F07.G"
                     /sex="mixed pool"
                     /dev_stage="schistosomulum"
                     /lab_host="in vitro culture"
                     /clone_lib="MS1-0011"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 14;  Length 329;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||| ||| ||||| |||||
Db        278 TCGTCTAACCTTCGACATGAT 258


RESULT 33
CD092357/c
LOCUS       CD092357                342 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  MC1-0096T-D093-B07-U.G MC1-0096 Schistosoma mansoni cDNA clone
            MC1-0096T-D093-B07.G, mRNA sequence.
ACCESSION   CD092357
VERSION     CD092357.1  GI:34643083
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: MC1-0096T-D093  row: 7  column: B.
FEATURES             Location/Qualifiers
     source          1. .342
                     /organism="Schistosoma mansoni"
                     /mol_type="mRNA"
                     /db_xref="taxon:6183"
                     /clone="MC1-0096T-D093-B07.G"
                     /sex="mixed pool"
                     /dev_stage="cercaria"
                     /lab_host="Biomphalaria glabrata"
                     /clone_lib="MC1-0096"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 14;  Length 342;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||||| || ||||| ||||
Db        131 TCGTCGATCGATCGAGTTGAT 111


RESULT 34
AQ840347
LOCUS       AQ840347                374 bp    DNA     linear   GSS 01-SEP-1999
```

```
DEFINITION  nbxb0055D20f CUGI Rice BAC Library Oryza sativa (japonica
            cultivar-group) genomic clone nbxb0055D20f, genomic survey
            sequence.
ACCESSION   AQ840347
VERSION     AQ840347.1  GI:5818400
KEYWORDS    GSS.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 374)
  AUTHORS   Wing,R.A. and Dean,R.A.
  TITLE     A BAC End Sequencing Framework to Sequence the Rice Genome
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: TAATACGACTCACTATAGGG
            Class: BAC ends
            High quality sequence stop: 314.
FEATURES             Location/Qualifiers
     source          1. .374
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="genomic DNA"
                     /strain="Japonica"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="nbxb0055D20f"
                     /tissue_type="Leaf"
                     /lab_host="E. coli DH10B"
                     /clone_lib="CUGI Rice BAC Library"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                     HindIII; Rice is one of two most popular grains in the
                     world. Half of the world  population especially those
                     inhabiting highly populated areas of the  humid tropics
                     and subtropics, rely on rice as their primary source of
                     carbohydrate. Monocotyledonous rice is a diploid plant
                     (2n=24) with a  haploid genome equivalent of 431 Mbp
                     (Arumuganathan and Earle, 1991).  The relatively small
                     genome of rice, three times larger than that of
                     Arabidopsis, makes it suitable for genomic studies. In
                     order to  facilitate positional cloning, physical mapping
                     and genome sequencing  of rice, we have constructed a BAC
                     library from Oryza sativa, Nipponbare  variety. The
                     library contains 36,864 clones with an average insert size
                     of 128.5 Kb providing 10.9 haploid genome equivalents. The
                     deep  coverage allows the isolation a particular sequence
                     with a probability  of 99.9 %. Two high density filters,
                     each containing 18,432 clones  (doubly spotted), represent
                     the whole library for colony screening."
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 28;  Length 374;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              | ||| ||||||||| |||||
Db        180 TTGTCAAACGTTCGATATGAT 200


RESULT 35
CD190376/c
LOCUS       CD190376                375 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  MS1-0064U-A245-H12-U.B MS1-0064 Schistosoma mansoni cDNA clone
            MS1-0064U-A245-H12.B, mRNA sequence.
ACCESSION   CD190376
VERSION     CD190376.1  GI:34720349
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 375)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: MS1-0064U-A245  row: 12  column: H.
FEATURES             Location/Qualifiers
     source          1. .375
                     /organism="Schistosoma mansoni"
                     /mol_type="mRNA"
                     /db_xref="taxon:6183"
                     /clone="MS1-0064U-A245-H12.B"
                     /sex="mixed pool"
                     /dev_stage="schistosomulum"
                     /lab_host="in vitro culture"
                     /clone_lib="MS1-0064"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 14;  Length 375;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              | ||| ||||||||| |||||
Db        116 TCGTCTAACTTTCGACATGAT 96


RESULT 36
CD178552/c
LOCUS       CD178552                377 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  MS1-0014P-A231-C01-U.B MS1-0014 Schistosoma mansoni cDNA clone
            MS1-0014P-A231-C01.B, mRNA sequence.
ACCESSION   CD178552
VERSION     CD178552.1  GI:34709002
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 377)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
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            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: MS1-0014P-A231  row: 1  column: C.
FEATURES              Location/Qualifiers
     source           1. .377
                      /organism="Schistosoma mansoni"
                      /mol_type="mRNA"
                      /db_xref="taxon:6183"
                      /clone="MS1-0014P-A231-C01.B"
                      /sex="mixed pool"
                      /dev_stage="schistosomulum"
                      /lab_host="in vitro culture"
                      /clone_lib="MS1-0014"
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 14;  Length 377;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              || || |||| ||||||||||
Db        140 TCATCAAACGGTCGAGATGAT 120


RESULT 37
CD187006/c
LOCUS       CD187006                384 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  MS1-0056U-V332-D10-U.B MS1-0056 Schistosoma mansoni cDNA clone
            MS1-0056U-V332-D10.B, mRNA sequence.
ACCESSION   CD187006
VERSION     CD187006.1  GI:34717091
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: MS1-0056U-V332  row: 10  column: D.
FEATURES              Location/Qualifiers
     source           1. .384
                      /organism="Schistosoma mansoni"
                      /mol_type="mRNA"
                      /db_xref="taxon:6183"
                      /clone="MS1-0056U-V332-D10.B"
                      /sex="mixed pool"
                      /dev_stage="schistosomulum"
                      /lab_host="in vitro culture"
                      /clone_lib="MS1-0056"
                      /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 14;  Length 384;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||| ||| ||||| |||||
Db        136 TCGTCTAACTTTCGACATGAT 116


RESULT 38
CD190545/c
LOCUS       CD190545                384 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  MS1-0064U-A263-D10-U.B MS1-0064 Schistosoma mansoni cDNA clone
            MS1-0064U-A263-D10.B, mRNA sequence.
ACCESSION   CD190545
VERSION     CD190545.1  GI:34720515
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: MS1-0064U-A263  row: 10  column: D.
FEATURES              Location/Qualifiers
     source           1. .384
                      /organism="Schistosoma mansoni"
                      /mol_type="mRNA"
                      /db_xref="taxon:6183"
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                     /clone="MS1-0064U-A263-D10.B"
                     /sex="mixed pool"
                     /dev_stage="schistosomulum"
                     /lab_host="in vitro culture"
                     /clone_lib="MS1-0064"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 14;  Length 384;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||| ||| ||||| |||||
Db        135 TCGTCTAACTTTCGACATGAT 115


RESULT 39
CD124011/c
LOCUS       CD124011                 392 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  ME1-0084T-L228-D07-U.B ME1-0084 Schistosoma mansoni cDNA clone
            ME1-0084T-L228-D07.B, mRNA sequence.
ACCESSION   CD124011
VERSION     CD124011.1  GI:34662045
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 392)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
  MEDLINE   22879926
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, Q5508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: ME1-0084T-L228  row: 7  column: D.
FEATURES             Location/Qualifiers
     source          1. .392
                     /organism="Schistosoma mansoni"
                     /mol_type="mRNA"
                     /db_xref="taxon:6183"
                     /clone="ME1-0084T-L228-D07.B"
                     /sex="mixed pool"
                     /dev_stage="egg"
                     /lab_host="Mus musculus"
                     /clone_lib="ME1-0084"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 14;  Length 392;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              ||||| ||| ||||| |||||
Db        278 TCGTCTAACTTTCGACATGAT 258


RESULT 40
AW699669/c
LOCUS       AW699669                 410 bp    mRNA    linear   EST 18-APR-2000
DEFINITION  gb30d06.y1 Moss EST library PPN Physcomitrella patens cDNA clone
            PEP_SOURCE_ID:PPN140212 5' similar to gb:emb|Z23165.1|ATRBPS18A
            A.thaliana ribosomal protein gene (PLANT);, mRNA sequence.
ACCESSION   AW699669
VERSION     AW699669.1  GI:7583764
KEYWORDS    EST.
SOURCE      Physcomitrella patens
  ORGANISM  Physcomitrella patens
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
            Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE   1  (bases 1 to 410)
  AUTHORS   Quatrano,R., Bashiardes,S., Cove,D., Cuming,A., Knight,C.,
            Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T.,
            Underwood,K., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Steptoe,M., Gibbons,M., Harvey,N., Ritter,E.,
            Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
  TITLE     Leeds/Wash U Moss EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Ralph Quatrano
            Leeds/Wash U Moss EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Libraries were constructed by Dr. Stavros Bashiardes as part of the
            Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
            Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
            Seq primer: -40RP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .410
                     /organism="Physcomitrella patens"
                     /mol_type="mRNA"
                     /db_xref="taxon:3218"
                     /clone="PEP_SOURCE_ID:PPN140212"
                     /tissue_type="protonemata: 7 day old tissue auxin treated"
                     /lab_host="DH10B"
                     /clone_lib="Moss EST library PPN"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; Construction of the cDNA library was carried out
                     using Stratagenes 'UniZAP - cDNA synthesis kit'.  cDNA was
                     constructed using an oligo dT primer/linker that contains
                     a XhoI site within it.  Following ds cDNA  synthesis,
                     EcoRI adapters were ligated to the blunt ends and sample
                     was digested with XhoI. The result is cDNA with an EcoRI
                     sticky end on one side and a XhoI sticky end on the other.
                     This cDNA was ligated directionally in UniZAP arms. The
                     vector is designed containing the pBluescript sequence as
                     well as lambda DNA and cDNA is cloned within this
                     pBluescript sequence. The vector was then packaged using
                     Gold gigapackaging extracts. Library was grown in XLIBlue
                     MRF' cells and amplified. The library was excised by mass
                     excision using Stratagens 'Mass excision kit' that uses
                     exassist as a helper phage that releases the pBluescript
                     sequence and circularises it as single stranded plasmids
                     that are then packaged (by helper phage) and secreted out
                     of the host cell as phagemids. SOLR cells were transformed
                     with phagemids and the library was plated out on LB-amp
                     plates to select for transformants. Approximately
                     1,000,000 colonies were grown and recovered. The double
                     stranded plasmid library was recovered by using Quiagen
                     Midi prep kit. 2 micro grams of each library were used to
                     transform DH10B cells by electroporation."
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ORIGIN

Query Match 77.1%; Score 16.2; DB 10; Length 410;
Best Local Similarity 85.7%; Pred. No. 2.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 TCGTCGAACGTTCGAGATGAT 21
              || || |||||||||||| ||
Db         87 TCTTCAAACGTTCGAGATCAT 67
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